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Factors affecting the accuracy of selection indexes for the genetic improvement of pigs

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Factors affecting the accuracy of selection indexes for the genetic improvement of pigs

by

Walter Michel Vandepitte

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TABLE OF CONTENTS

LIST OF TABLES

LIST OF FIGURES

I. INTRODUCTION

Most of the research work in animal breeding in the past has been mainly concerned with parameter estimation, methods of genetic evaluation and the nature of response to selection. Research leading to complete definition of realistic selection goals does not seem to have been very adequate.

Historically, the selection index introduced to animal breeding work by Hazel (1943) has been an extremely significant contribution not only for the genetic aspects of animal breeding but also for the economic aspects. The "relative economic weight" defined by Hazel as "the amount by which profit may be expected to increase for each unit of improvement in that trait" appears to be the first formalized attempt to combine genetic and economic information in an index useful for decision-making in multiple trait selection.

The selection index theory is finding increasing use in recent years, due to the relative ease with which indexes can be calculated by computer. Many studies have extended index theory (Le Roy, 1955; Henderson, 1963; Wilton et al., 1968; Wilton and Van Vleck, 1969; Van Vleck, 1970) and clarified particular aspects such as restricted indexes (Kempthorne and Nordskog, 1959; and Cunningham, 1969) and the influence of errors in the parameter estimation (Harris, 1961; Williams, 1962a and 1962b; and Heidhues, 1961). However, little attention has been given to the economic aspects of the selection index, namely the estimation of the economic weights and the effect of errors in economic weights on the efficiency of the index.

Information on noneconomic traits or on economic traits of animals subject to selection may increase the accuracy of index selection, but have less clearly realized detrimental effects. For example, intense testing may reduce the number of animals tested, thereby reducing the selection differential. Or testing over a longer period may increase accuracy, but less than can be compensated for by the increased generation interval.

In this study attention is primarily toward the effects of errors in the economic weights and the utility of combinations of information as they relate to the rate of genetic change which can be achieved by index selection.

II. REVIEW OF LITERATURE

The review of literature of this study will be divided in three parts: economic aspects of animal breeding, selection index theory, and the effect of errors in the parameters.

A. Economic Aspects of Animal Breeding

1. Technological change

In all the work that has been published in the field of economics of research and development and technological change, the topic of genetic improvement of domestic animals has never been covered explicitly. However, some useful thoughts were developed by Zvi Griliches (1957) in his study about technological change with respect to Hybrid Corn. He developed a mathematical model for the supply of a new technique and discussed the rate of acceptance and the equilibrium level of use. The effect on farmers' income and consumer spending was not discussed. W. L. Peterson (1967) used two different methods (the index number approach and the production function approach) to evaluate the return to poultry research in the United States. The effect of research in breeding, nutrition and management were not considered separately. The effect of production increase by technological change in animal production has been studied by Zeddies and Weniger (1970a). Discussing price mechanism and evolution of farm income, they conclude that in the long run, depending on the elasticity of demand and supply, the social return from technological change goes mainly to the consumer, distribution and transformation sector takes the second fraction and the third (by far the smallest)

fraction goes to the farmer-producer. Heady (1961) discussed in very general terms the effect of technological improvement and education on farm income and economic growth, and stated that "public research and education for technological improvement in its present form is a food policy element and not a farm policy element."

2. Economic evaluation of selection schemes

In recent years animal breeding research workers are showing increasing interest in the economic aspects of animal breeding. Several attempts have been made to provide a total economic evaluation of selection programs. Strain (1961) developed profit functions and evaluated the importance of the rate of egg production and adult body weight in integrated and nonintegrated poultry operations. Swanson (1965) developed profit equations for sheep enterprises. He also calculated the effect of changes of profit potential for different operations as production changed. Smith (1964), and Moav and Moav (1966) showed that any expression of profitability of a crossbred must be a function of the reproductive performance of the parents and the productive efficiency and quality of their offspring. Moav (1966a) explored the economic considerations in developing specialized sire and dam lines. He developed general expressions for profitability of the crossbreds. This expression for net profit included gross income, production cost, and reproduction cost. He further showed how the genotype of sire, dam and crossbred offspring affected the components of the profit function. When different numbers of males and females are needed, the contributions of the parental lines are not equal. He suggested that the exploitation of this difference may

produce "profit heterosis" even if the component traits are genetically additive.

Moav (1966b), Moav (1966c) and Moav and Hill (1966) investigated this situation under different genetic conditions and drew conclusions about the most profitable choices of parental lines for each case. Jakubec and Fewson (1970) expanded Moav's theory with respect to heterosis effects and different three and four line cross schemes. In an attempt to maximize the economic efficiency by selection Zeddies and Weniger (1970b) used linear programming techniques to select the appropriate selection index, testing method and selection intensity subject to limited budget and testing capacity. Touchberry (1970) used an economic analysis of a Holstein and Guernsey crossbreeding project to demonstrate that the increase in viability increased income as well as the potential culling intensity which could be a major factor in increasing genetic gain. Pearson (1971) delivered a significant contribution to the complete economic evaluation of a dairy cattle breeding program by determining the most profitable cow culling system and age distribution. An investment appraisal for national breeding programs in Great Britain was worked out by Hill (1971).

B. Selection Index Theory

1. The construction of a selection index

The objective of selection will always be to affect population changes in one or more traits which relate to the economic value of the members of the population. Whatever these traits may be, one can always express the

net economic worth or net profit of an animal (W_j) as a function of these traits ($x_1, x_2, \ldots, x_n$).

$$W_j = a_1x_{1j} + a_2x_{2j} + \ldots + a_nx_{nj} + e_j \qquad j = 1, \ldots, N \tag{1}$$

Where $a_1, a_2, \ldots, a_n$ are the partial multiple regression coefficients from the regression of net profit on the phenotypic values $x_1, x_2, \ldots x_n$ and e_j is an error term. Notice that $W_j = f(x_{ij})$ does not have to be linear in the x_{ij}'s. The estimated profitability is (we will drop the j subscripts)

$$\hat{W} = \hat{a}_1x_1 + \hat{a}_2x_2 + \ldots + \hat{a}_nx_n \quad . \tag{2}$$

The a_i's are exactly the economic weights, defined by Hazel (1943) as " ... the amount by which net profit may be expected to increase for each unit of improvement in that trait." Under the additivity assumption $x = g + e$ (phenotypic value is equal to an additive genetic component and an environmental component), we can rewrite (2) as

$$\hat{W} = \hat{a}_1(g_1 + e_1) + \hat{a}_2(g_2 + e_2) + \ldots + \hat{a}_n(g_n + e_n) \; . \tag{3}$$

If we define

$$\hat{H} = \hat{a}_1g_1 + \hat{a}_2g_2 + \ldots + \hat{a}_ng_n \qquad \text{and} \tag{4}$$

$$\hat{E} = \hat{a}_1e_1 + \hat{a}_2e_2 + \ldots + \hat{a}_ne_n$$

$\hat{W}$ becomes

$$\hat{W} = \hat{H} + \hat{E} \; .$$

Where $\hat{H}$ is the complete average genetic net worth or complete aggregate genotype and $\hat{E}$ is the deviation from the complete average genetic net worth associated with the particular environment in which the phenotype is observed. $\hat{H}$ is a linear function of n nonobservable variables and is the quantity to be improved by selection. The most efficient selection criterion I (selection index) is the one having the largest possible correlation with $\hat{H}$ (Hazel, 1943). An obvious index would be $\hat{W}$ itself as illustrated by Manning (1956). However the x_i values in $\hat{W}$ are not always measurable on the individual. Or for practical reasons we may direct our attention to traits that have indirectly a unique significance with respect to yield or quality. For this reason an index of the form

$$I = \beta_1 x_1 + \beta_2 x_2 + \ldots + \beta_m x_m \qquad (5)$$

can be considered, where $x_1, x_2, \ldots, x_m$ are representing objective measurements or numerical scores on the individual and or its relatives, and $\beta_1, \beta_2, \ldots, \beta_m$ are constants obtained as solutions from a set of simultaneous equations (this will be clarified later). Notice that for practical reasons one might be interested in improving only a subset of $\hat{H}$, say $\hat{\hat{H}}$ (reduced aggregate genotype), where

$$\hat{\hat{H}} = \hat{a}_1 g_1 + \hat{a}_2 g_2 + \ldots + \hat{a}_t g_t \text{ with } t \leq n \; . \qquad (6)$$

There is some confusion in the literature and even among researchers about the definition of economic weights. I believe that Hazel's definition is the only correct one. Confusion arose because the net profit function $\hat{W}$, and the relationship between the net profit function and the

aggregate genotype $\hat{H}$ was not exhibited in the papers of Smith (1936) and Hazel (1943). Sometimes the economic weights are incorrectly defined as partial multiple regression coefficients from the regression of aggregate genotype $\hat{H}$ on the genetic values g_i. However the genetic values g_i are unknown and the usual procedure is to calculate the economic weights based upon phenotypic values. Since the genetic values g_i and the phenotypic values x_i have a different variance-covariance structure, it is easy to verify that the estimates obtained by this procedure are in contradiction with the definition. The necessary and sufficient conditions that these two definitions of economic weights yield the same index coefficients β_i are that a) the $\hat{E}$ equals zero and b) that $\hat{W}$ and $\hat{H}$ concontain the same set of traits.

The magnitude of R(IH), the correlation between the aggregate genotype and the index, provides a criterion for choice among indexes. In what follows we will use the symbol H for $\hat{H}$ and $\hat{\hat{H}}$.

Smith (1936) and Hazel (1943) demonstrated that the optimum estimates for β_i, are functions of a) the genetic and phenotypic variances and covariances of the traits in I and H and b) the relative economic weights. A least squares procedure can be used to obtain the β_i's. Minimizing $E(I - H)^2$ by differentiating

$$\frac{1}{2} \frac{\partial E(I - H)^2}{\partial \beta_i} = 0$$

will yield the following simultaneous equations:

$$\hat{\beta}_1\sigma x_1x_1 + \hat{\beta}_2\sigma x_1x_2 + \ldots + \hat{\beta}_m\sigma x_1x_m = \sigma x_1H$$

$$\hat{\beta}_1\sigma x_2x_1 + \hat{\beta}_2\sigma x_2x_2 + \ldots + \hat{\beta}_m\sigma x_2x_m = \sigma x_2H$$

$$\cdot \qquad \cdot \qquad \ldots \qquad \cdot \quad = \quad \cdot$$

$$\hat{\beta}_1\sigma x_mx_1 + \hat{\beta}_2\sigma x_mx_2 + \ldots + \hat{\beta}_m\, x_mx_m = \sigma x_mH \qquad (7)$$

$$\sigma x_1H = \hat{a}_1\sigma g_1g_1 + \hat{a}_2\sigma g_1g_2 + \ldots + \hat{a}_n\sigma g_1g_n$$

$$\sigma x_2H = \hat{a}_1\sigma g_2g_1 + \hat{a}_2\, g_2g_2 + \ldots + \hat{a}_n\sigma g_2g_n$$

$$\cdot \quad = \quad \cdot \quad + \quad \cdot \quad + \ldots + \quad \cdot$$

$$\sigma x_mH = \hat{a}_1\sigma g_mg_1 + \hat{a}_2\sigma g_mg_2 + \ldots + \hat{a}_n\sigma g_mg_n$$

Where σx_ix_i is the phenotypic variance of x_i $\quad i = 1, \ldots, m$

σx_ix_j is the phenotypic covariance of x_i and x_j for $i \neq j$

σg_ig_j is the covariance between x_i and g_j with

$i = 1, \ldots, m$ and $j = 1, \ldots, n$

$\hat{a}_i$ is the economic weight of the i^{th} trait in the aggregate genotype. These parameters are assumed to be the appropriate values of the popuiation for which the index is calculated. The simultaneous equations can be solved for β_i and will give the optimal index I on which selection will be based. Maximizing R(IH) (the correlation between index and aggregate genotype) by differentiating $\frac{\partial \log\,(R(IH))}{\partial \beta_i} = 0$ yields

equivalent solutions for the $\hat{\beta}_i$'s. This also maximizes expected genetic gain and the probability of correct selection, because both are monoconically increasing functions of this correlation. For convenience, we will now proceed in matrix notation. The information required in constructing a selection index can be specified by the following vectors and matrices:

$g = g_1, \ldots, g_n$	is a vector of unknown additive genetic values for the n traits included in the aggregate genotype.
$a = a_1, \ldots, a_n$	is a vector representing the relative economic values of the n traits in H.
$p = x_1, \ldots, x_m$	is a vector of phenotypic measures for the m sources of information to be included in the index.
$b = b_1, \ldots, b_m$	is a vector of unknown weighting factors to be used in the index.
P	is a m x m matrix of phenotypic covariances between the m variables in p.
G	is a m x n matrix of genotypic covariances between the m variables in p and the n traits in H.
C	is a n x n matrix of genotypic covariances between the n traits in g.

The aggregate genotype is defined as $H = a'g$. Since H is not measurable we cannot select for it directly. Improvement in H is brought about by

selection on an index or selection criterion.

$$I = b'p$$

The b_i coefficients in I are obtained by solving the following simultaneous equations

$$Pb = Ga \tag{8}$$

to give

$$b = P^{-1}Ga \quad . \tag{9}$$

The variance of the index, the variance of the aggregate genotype and the covariances of index and aggregate genotype are

$$\sigma I^2 = b'Pb \tag{10}$$

$$\sigma H^2 = a'Ca \tag{11}$$

$$\sigma HI = b'Ga = b'Pb \quad . \tag{12}$$

The correlation between the index and the aggregate genotype can be factored as follows:

$$R(HI) = \frac{\sigma HI}{\sigma H \sigma I} = \frac{\sigma I}{\sigma H} = \sqrt{\frac{b'Ga}{a'Ca}} \tag{13a}$$

R(HI) can also be expressed as computed from the simultaneous equation (7)

$$R(HI) = \left[\frac{\Sigma b_i (RHS)_i}{\sigma H^2} \right]^{1/2} \tag{13b}$$

Where $(RHS)_i$ refers to the righthand side of the i^{th} equation. The expected genetic gain in H for truncation selection in a normal distribution

is then

$$\Delta H = iR(HI)\sigma H = i\sigma I = i\sqrt{b'Pb} \quad . \tag{14}$$

Where i is the selection differential in I. The genetic gain in trait j can be calculated using the regression of trait j on the index or the correlation between trait j and the index. The regression of trait j on I is

$$b(G_j I) = \frac{b'G_j}{b'Ga} \tag{15}$$

where G_j is the j^{th} column vector of G. The correlation of trait j with I is

$$R(G_j I) = \frac{b'G_j}{\sqrt{(b'Ga)(C_{jj})}} \tag{16}$$

where C_{jj} is the j^{th} diagonal element of C. The genetic gain in trait j is then

$$\Delta G_j = i\, b(G_j I)\sigma I = i\, \frac{b'G_j}{\sqrt{b'Ga}} \quad . \tag{17}$$

The economic value of the gain in trait j relative to the total gain ΔH can be calculated as follows

$$\text{val. } \Delta G_j = a_j \Delta G_j = i\, b(G_j I)\sigma I a_j \tag{18}$$

and

$$\Delta H = \sum_j a_j \Delta G_j = i\, \sigma I \sum_j a_j\, b(G_j I)$$

If $\Delta H = i\, \sigma I$, the economic value of the genetic gain in G_j (expressed as percent of ΔH) resulting from selection on index I is then

$$\text{Rel. Ec. val. } \Delta G_j = \frac{b'G_j}{b'Ga} a_j \, 100. \tag{19}$$

It can be useful to calculate the subindexes following Henderson (1963). The procedure is equivalent to the methods previously described but is more adaptable to conditions where changes in economic values occur or where it may be desirable to compare alternative sets of economic values. The index is obtained as follows

$$I = \sum_j a_j I_j \tag{20}$$

where I_j is the subindex of the j^{th} trait. The index weight b_k is then computed by

$$b_k = \sum_j a_j b_{kj} \, . \tag{21}$$

2. Selection indexes for a nonlinear aggregate genotype

As mentioned previously the profit function $\hat{W}$ is not necessarily linear in the x_i's, nor has H to be linear in the g_i's. There are cases in which linear models are not valid, as pointed out by Kempthorne (1957) and Dickerson (1960). In some cases the economic value of one trait depends on the level of some other trait, and in other cases the economic value of a trait may not be linear. An example of the first type is market weight and carcass grade in beef cattle and an example of the second type could be backfat thickness in pigs.

Quadratic indexes have been developed by Wilton et al. (1968) and calculated by Wilton and Van Vleck (1969). Quadratic and cubic models have been worked out by Rønningen (1971a). However, the topic of non-linear selection indexes seems to have only academic interest, because in the few cases where a nonlinear index was calculated, a linear index was practically as efficient and, in addition, was much simpler. The aggregate genotype here considered is

$$H = a'(\mu + g) + a_s'(\mu + g)_s + a_c'(\mu + g)_c \qquad (22)$$

in which

H	is the aggregate genotype as defined earlier
$(\mu + g)$	is a n x 1 vector of genetic values of the traits under consideration, assumed to be distributed as $N(\mu,C)$, with μ being a vector of population means, g a vector of deviations of the genetic values from the means, and C the n x n variance covariance matrix.
$(\mu + g)_s$	is a n x 1 vector of the genetic values squared
$(\mu + g)_c$	is a $1/2n(n - 1)$x 1 vector of cross-products of any two traits
a	is a n x 1 vector of economic weights
a_s	is a n x 1 vector of economic weights applying to the genetic values squared, and
a_c	is a $1/2n(n - 1)$x 1 vector of economic weights applying to the cross products between the genetic values of any two traits.

Model (22) can then be rearranged in

$$H = a'(\mu + g) + (\mu + g)'A(\mu + g) \qquad (23)$$

in which A is a n x n matrix of the form

$$\begin{matrix} a_{11} & 1/2a_{12} & \cdots & 1/2a_{1n} \\ 1/2a_{21} & a_{22} & \cdots & 1/2a_{2n} \\ \cdot & \cdot & \cdots & \cdot \\ 1/2a_{n1} & 1/2a_{n2} & \cdots & a_{nn} \end{matrix}$$

With a_{ii} being the relative economic weight of the genetic value of the i^{th} trait squared, and a_{ij} the relative economic weight of the cross-products between the genetic values of the i^{th} and the j^{th} trait. Now a linear index or a quadratic index can be considered as selection criterion when the aggregate genotype is quadratic.

a. Linear index The linear index can be defined as

$$I = \alpha + b'p \qquad (24)$$

in which

I is the linear index

α is a constant

p is a m x 1 vector of phenotypic observations, expressed as deviations from their means, and distributed as N(0, P), with P being the m x m matrix of phenotypic variances and

covariances. p is assumed to have a covariance matrix G with g, and

b is a m x 1 vector of index coefficients.

The b's will be estimated as usual by minimizing the squared difference between aggregate genotype and index, both expressed as deviations from their expectations. That is $E\{[I - E(I)] - [H - E(H)]\}^2$ is minimized. $[I - E(I)] = b'p$, since the elements of p are expressed as deviations.

$$[H - E(H)] = (\mu + g)'a + (\mu + g)'A(\mu + g) - [\mu'a+\mu'A\mu+tr(AC)]$$

$$= g'a + 2g'A\mu + g'Ag - tr(AC)$$

In which tr denotes the trace of a matrix. The expectation of the squared difference becomes

$$E\{[I - E(I)] - [H - E(H)]\}^2 = E[p'b-g'a-2g'A\mu-g'Ag+tr(AC)]^2$$

$$= E[b'pp'b-2b'pg'a-4b'pg'A\mu-2b'pg'Ag+2b'ptr(AC) + \text{terms not including b}]$$

$$= b'Pb-2b'Ga-4b'GA\mu+E[\text{terms not including b}] . \qquad (25)$$

The E(pg'Ag) in the previous expression is zero, since it involves the product of three normally distributed variables with zero mean. Differentiating (25) with respect to b and equating to zero yields

$$2Pb - 2Ga + 4GA\mu$$

so that $b = P^{-1}G(a+2A\mu)$.

The linear index is thus

$$I = \alpha + p' [P^{-1}G(a + 2A\mu)] . \qquad (26)$$

The only additional information that is required to construct a linear index for a quadratic aggregate genotype are the relative economic weights (matrix A). The special case when $A = \phi$, a null matrix, and $\alpha = 0$, results in the normal linear index $I = p'P^{-1}Ga = p'b$. The covariance between quadratic aggregate genotype and linear index is

$$\begin{aligned}\sigma HI_{\ell} &= E[I_{\ell} - E(I_{\ell})][H-E(H)] \\ &= E(b'p)(g'a+2g'A\mu+g'Ag+tr(AC)) \\ &= b'Ga+2b'GA\mu = b'G(a+2A\mu) \ .\end{aligned}$$

The variance of the linear index is

$$\begin{aligned}\sigma^2 I_{\ell} &= E(I_{\ell}-E(I_{\ell}))^2 \\ &= b'Pb = b'G(a+2A\mu).\end{aligned}$$

Thus $\sigma HI_{\ell} = \sigma^2 I_{\ell}$ and the variance of a quadratic aggregate genotype is

$$\begin{aligned}\sigma^2 H &= E(H-E(H))^2 \\ &= E(a'g+2\mu'Ag+g'Ag-tr(AC))^2 \\ &= a'Ca+4a'CA\mu+4\mu'ACA\mu+2tr(ACAC).\end{aligned}$$

b. Quadratic index A quadratic index considers squares and cross-products of phenotypic deviations as well as the phenotypic deviations themselves and is defined as

$$I = \alpha + b'p + b_s'p_s + b_c'p_c \qquad (27)$$

in which

I is the quadratic index

α is a constant

p is a m x 1 vector of phenotypic deviations as described for the linear index

p_s is a m x 1 vector of squared phenotypic deviations

p_c is a 1/2m(m-1)x1 vector of cross-products of phenotypic deviations

b is a m x 1 vector of weights for the phenotypic deviations

b_s is a m x 1 vector of weights for the squared phenotypic deviations and

b_c is a 1/2m(m-1)x1 vector of weights for the cross-products of phenotypic deviations

b, b_s and b_c are the index coefficients obtained as solutions of the simultaneous equations.

This index can be rewritten as $I = \alpha + b'p + b'Bp$, in which B is a m x m matrix of the form

$$\begin{matrix} b_{11} & 1/2b_{12} & \cdots & 1/2b_{1m} \\ 1/2b_{21} & b_{22} & \cdots & 1/2b_{2m} \\ \cdot & \cdot & \cdots & \cdot \\ 1/2b_{m1} & 1/2b_{m2} & \cdots & b_{mm} \end{matrix}$$

with b_{ii} being the selection index weight for the square of the i^{th} phenotypic deviation and b_{ij} being the selection index weight for the cross-product of the i^{th} and the j^{th} phenotypic deviation. Using the same criterion as for a linear index, we obtain

$$
\begin{aligned}
& E[(I-E(I)) - (H-E(H))]^2 \\
= \; & E[\alpha+b'p+p'Bp-(\alpha+tr\,BP))-(g'a+2g'A\mu+g'Ag-tr(AC))]^2 \\
= \; & E[b'pp'b+2b'pp'Bp-2b'ptr(BP)-2b'pg'a-4b'pg'A\mu \\
& - 2b'pg'Ag+2b'ptr(AC)+p'Bpp'Bp-2p'Bptr(BP)-2p'Bpg'a \\
& - 4p'Bpg'A\mu-2p'Bpg'Ag+2p'Bptr(AC)+tr(BP)tr(BP)+2tr(BP)g'a \\
& + 4tr(BP)g'A\mu-2p'Bpg'Ag+2p'Bptr(AC)+tr(BP)tr(BP) \\
& + 2tr(BP)g'a+4tr(BP)g'A\mu+2tr(BP)g'Ag-2tr(BP)tr(AC) \\
& + \text{terms not involving } b \text{ or } B]. \qquad (28)
\end{aligned}
$$

The terms involving b are exactly the same as in the linear index. The terms involving b and B are the products of three normally distributed random variables with mean zero so that their expectations are zero. The terms involving B have expectations

$$
\begin{aligned}
& E(p'Bpp'Bp) = Var(p'Bp)+tr(BP)tr(BP) \\
& \qquad = 2tr(BPBP)+tr(BP)tr(BP) \\
& E(-2p'Bptr(BP)) = -2tr(BP)tr(BP) \\
& E(-2p'Bpg'a) = 0 \\
& E(-4p'Bpg'A\mu) = 0 \\
& E(-2p'Bpg'Ag) = -2Cov(p'Bp,g'Ag) - 2tr(BP)tr(AC) \\
& \qquad = -4tr(BGAG') - 2tr(BP)tr(AC), \text{ for p and g} \\
& \qquad \text{normal distributed, from Searle (1958)} \\
& E(2p'Bptr(AC)) = 2tr(BP)tr(AC) \\
& E(tr(BP)tr(BP)) = tr(BP)tr(BP) \\
& E(tr(BP)g'a) = 0 \\
& E(4tr(BP)g'A\mu) = 0
\end{aligned}
$$

$$E(2tr(BP)g'AG) = 2tr(BP)tr(AC)$$

$$E(-2tr(BP)tr(AC)) = -2tr(BP)tr(AC)$$

Summing the expectations of terms involving B gives

$$2tr(BPBP) - 4tr(BGAG') \tag{29}$$

Therefore the expectation of (28) is

$$b'Pb-2b'Ga-4b'GA\mu+2tr(BPBP)-4tr(BGAG') \tag{30}$$

Differentiating (30) with respect to b and equating to zero gives

$$2Pb - 2G(a+2A\mu) = 0$$

and differentiating (30) with respect to B and equating to zero gives

$$4PBP - 4GAG' = 0$$

therefore,

$$b = P^{-1}G(a+2A\mu)$$

$$B = P^{-1}GAG'P^{-1}$$

The quadratic index is then

$$I = \alpha+p'b+p'Bp$$

$$= \alpha+p'P^{-1}G(a+2A\mu)+p'P^{-1}GAG'P^{-1}p \ . \tag{31}$$

Again if $A = \phi$ and $\alpha = 0$ we obtain the simple linear index. The covariance between a quadratic aggregate genotype and a quadratic index is

$$\sigma HI_q = E(I_q - E(I_q)(H - E(H))$$

$$= b'G(a + 2A\mu) = 2tr(BGAG')$$

and the variance of the quadratic index is

$$\sigma^2 I_q = b'Pb = 2tr(BPBP).$$

Thus $\sigma HI_q = \sigma^2 I_q$. Henderson (1963) has shown that under the assumption of normality, the maximum likelihood estimate of μ_i+g_i (the i^{th} element

of vector $\mu+g$) given the vector p is

$$\widehat{\mu_i + g_i}|p = S_i = \mu_i + p'b_i, \quad i = 1, \ldots, n \tag{32}$$

in which b_i is $P^{-1}G_i$ and G_i is the i^{th} column vector of G. If the m x 1 vector S is defined as the vector with the i^{th} element equal to S_i, the vector of maximum likelihood estimates is

$$\widehat{\mu + g}|p = S = \mu + G'P^{-1}p \ . \tag{33}$$

Making use of the invariance property of maximum likelihood estimates and substituting (33) in (22), the maximum likelihood estimate of H is

$$\begin{aligned}\hat{H}|p &= (\mu+G'P^{-1}p)'a + (\mu+G'P^{-1}p)'A(\mu+G'P^{-1}p) \\ &= \mu'a + \mu'A\mu + p'P^{-1}G(a+2A\mu) + p'P^{-1}GAG'P^{-1}p \ .\end{aligned} \tag{34}$$

Thus for α equal to $\mu'a+\mu'A\mu$, the quadratic index (31) is equivalent to the maximum likelihood estimate $\hat{H}|p$. This was proven by Wilton et al. (1968). For more theoretical details about nonlinear selection indexes we refer to Wilton et al. (1968) and Rønningen (1971a) and for calculated examples Wilton et al. (1968) and Wilton and Van Vleck (1969).

3. Restricted selection indexes

The idea of placing restrictions on selection indexes was introduced by Kempthorne and Nordskog (1959). They proposed that the normal equations be solved subject to the simultaneous conditions that the covariance between the index and a linear function of the genotypes involved be zero. Tallis (1962) extended this idea by equating the covariance to a predetermined constant so as to produce a graduated response in the genotypes. Rao (1962) gave methods for computing an index to improve one trait while

requiring that changes in other traits be of specified sign. James (1968) showed how restrictions could simultaneously be imposed on the genetic gains and on the index coefficients. In all cases, the equations carrying the restrictions were eliminated in solving for the index coefficients. Cunningham et al. (1970) presented a method to calculate restricted indexes, where the restricting equations are explicitly retained in the system.

a. Complete restriction Suppose that m traits, p_i, i=1, ..., m are to be used in a selection index $I = b'p$, and that ultimately r of these traits have reached an optimum and are to be kept on a constant level. A solution is obtained by minimizing $E(I-E(I))^2$ subject to the restriction $Cov(g_j,I) = 0$, j = 1, ..., r. Where $Cov(g_j,I)$ is the covariance between genotype g_j and index I. We have to minimize

$$\Phi = E(I-E(I))^2 + \sum_{j=1}^{r} 2\lambda_j b'G_j = 0 \qquad (35)$$

where λ_j is the j^{th} Lagrange Multiplier

$b'G_j$ is $Cov(g_j,I)$ where G_j is the j^{th} column vector of G.

Differentiating (35) with respect to b and λ we obtain the following matrix equations

$$\frac{1}{2}\frac{\partial\Phi}{\partial b} = Pb - Ga + G_r\lambda_r = 0 \qquad (36a)$$

$$\frac{1}{2}\frac{\partial\Phi}{\partial\lambda} = G'_r b = 0 \qquad (36b)$$

Where G_r is a matrix composed of r column vectors of G, corresponding to

the r traits one wants to restrict, and λ_r is a r x 1 vector of Lagrange Multipliers. Equation (36a) can be solved for b

$$b = P^{-1}(Ga - G_r\lambda_r)$$

and substituting this solution in (36b), we can solve for λ_r

$$\lambda_r = (G_r'P^{-1}G_r)^{-1}(G_r'P^{-1}Ga).$$

Substituting back into the b equation we get

$$b = [I - P^{-1}G_r(G_r'P^{-1}G_r)^{-1}G_r'] P^{-1}Ga \qquad (37)$$

This is the method used by Kempthorne and Nordskog (1959) and Tallis (1962). Equations (36) can also be rewritten as the following set of augmented normal equations in the form of partitioned matrices

$$\begin{bmatrix} P & G_r \\ \hline G_r' & \phi \end{bmatrix} \begin{bmatrix} b \\ \hline \lambda_r \end{bmatrix} = \begin{bmatrix} G \\ \hline \phi \end{bmatrix} \begin{bmatrix} a \\ \hline \phi \end{bmatrix} \qquad (38)$$

where ϕ is a null matrix. Or $P^*b^* = G^*a$ where the $(n+1)^{th}$ column of P^* consists of the j^{th} column of G for its first m elements, b^* is a $(n+r)x1$ vector of which the r last elements are Lagrange Multipliers and G^* is the original G matrix augmented by r rows of zeros. Also in the restricted index $I_r = b^{*\prime}p^*$, the p^* vector is augmented with r dummy variables, which take the value zero. This is the method used by Cunningham et al. (1970).

b. Partial restriction We may also want to restrict the genetic gain in trait j to a fraction or percentage k_j of the potential genetic gain.

$$\Delta g_j = \frac{\mathrm{Cov}(g_j, I)}{b'Pb}\,\Delta I = \alpha_j k_j \tag{39}$$

where ΔI is the selection differential and where we take α_j equal to $\Delta I/b'Pg$. This amounts to minimizing

$$\Phi = E(I-E(I))^2 + \sum_{j=1}^{r} 2\lambda_j (b'G_j - k_j) = 0 \tag{40}$$

When we differentiate (40) with respect to b and λ, we obtain the following equations

$$\frac{1}{2}\frac{\partial \Phi}{\partial b} = Pb - Ga + G_r\lambda_r = 0 \tag{41a}$$

$$\frac{1}{2}\frac{\partial \Phi}{\partial \lambda} = G_r'b - Ik = 0 \tag{41b}$$

These equations can be solved for λ_r and b, the final solution for b is

$$b = [I - P^{-1}G_r'(G_rP^{-1}G_r')^{-1}G_r]P^{-1}Ga + P^{-1}G_r'(G_rP^{-1}G_r')^{-1}k \,. \tag{42}$$

It is obvious that when k = 0 (42) is reduced to the complete restricted case (37), and in the degenerated case (r=0) we obtain the original simple linear index $b = P^{-1}Ga$. Equations (41) can be rewritten as partitioned matrices.

$$\left[\begin{array}{c|c} P & G_r \\ \hline G_r' & D_r \end{array}\right] \left[\begin{array}{c} b \\ \hline \lambda_r \end{array}\right] = \left[\begin{array}{c} G \\ \hline \phi \end{array}\right] \left[\begin{array}{c} a \\ \hline \phi \end{array}\right] \tag{43}$$

where D_r is a diagonal matrix with elements of the form $(-k_j/\lambda_j)$ with

$j = 1, \ldots, r$ in the diagonal.

In reality, however, the λ_r (Cunningham et al. (1970) calls them dummy weighting factors) are not known when the equations are being set up. The only way to solve these equations is to start with an estimate of λ_r and solve the equations iteratively. However, it might often be simpler to calculate indexes for several values of $(-k_j/\lambda_j)$ such that the effect of any degree of restriction can be obtained by interpolation. Notice also α_j from the condition Equation (39) is a function of the quadratic form $b'P^{-1}b$ and thus of the estimates themselves. If this is included in the conditions for minimization, the simultaneous equations are nonlinear in the b's, and there is no exact solution. For this reason we can only restrict $\mathrm{Cov}(g_j, I)$ and not Δg_j.

An alternative method for restricting genetic changes in a particular trait would be to use a suitable artificial economic weight in the aggregate genotype. The use of explicit restrictions will in general be preferable to manipulations of the economic weights since arbitrary economic weights give the aggregate genotype an arbitrary definition and make the prediction of genetic gain less useful. For applications of restricted indexes we refer to Kempthorne and Nordskog (1959) and Cunningham and Gjedrem (1970). Restricted index theory has been tested experimentally by Abplanalp et al. (1963) on turkeys, and by Okada and Hardin (1967) and Scheinberg et al. (1967) on Triboleum. The first two of these studies found good agreement with the theory. In the third, agreement was poor and the authors concluded that certain assumptions involved were not well founded.

4. Efficiency of selection indexes

It is useful to know the relative contribution of each variable in the index to the genetic progress for a defined aggregate genotype. The usual method for calculating the contribution of a particular variable is to construct a reduced index from which the variable in question has been excluded, and to compare the original and reduced indexes by means of their correlations with the aggregate genotype. Since genetic progress is proportional to the correlations, the comparison measures the relative value of the reduced index. When I_r is the reduced index, then the relative efficiency of the reduced index is given by

$$Reff = 100 \times \frac{R(HI_r)}{R(HI)} \quad . \tag{44}$$

The value of the i^{th} source of information in the original index can best be stated as the percent reduction in genetic progress which would result if that information was deleted. The loss in relative efficiency can be expressed as follows

$$LReff = 100\left(1 - \frac{R(HI_r)}{R(HI)}\right) \quad . \tag{45}$$

Using this method, one has to calculate a new index I_r of almost the same order as the first index. Based on the reduction of the index variance (σ^2_I), Cunningham (1969) proposed a faster and more convenient way to calculate the relative efficiency of a reduced index. When the i^{th} variable has been deleted the loss in efficiency is

$$LReff = 100\left[1-\sqrt{\frac{b'Pb-\frac{b_i}{w_{ii}}}{b'Pb}}\right] \qquad (46)$$

Where b_i is the i^{th} index coefficient and w_{ii} is the corresponding diagonal element of P^{-1}. If the i^{th} to j^{th} variables are deleted, b_i becomes a vector of the i^{th} to the j^{th} index coefficients from the original index and w_{ii} becomes the corresponding diagonal submatrix of P^{-1}. Having the inverse of P, one can easily calculate the relative value of each source of information.

The same ideas can be applied to calculate the relative efficiency of a linear index compared with a quadratic index when the aggregate genotype is quadratic (Wilton et al. 1968). When the effect of errors in the parameters (genotypic and phenotypic variances and covariances and economic weights) on genetic progress is studied, the concepts of relative efficiency and loss in relative efficiency are very useful. When ΔH is the expected genetic gain when all parameters are known and $\hat{I}$ is the index based on estimated parameters, the relative efficiency can be expressed as $(\Delta H|\hat{I}/\Delta H)$ where $(\Delta H|\hat{I})$ is the conditional genetic gain. Assuming that the selection intensities are equal $(i_1 = i_{\hat{1}})$ this is merely the ratio defined as the correlation of the index used (based on estimated parameters) with the correct aggregate genotype, divided by the correlation of the correct index with the correct aggregate genotype. It may also be of interest in some cases to look at the difference $\Delta H - (\Delta H|\hat{I})$.

C. Effect of Errors in the Parameters on Selection Indexes

In the selection index theory it is implicitly assumed that the genotypic and phenotypic parameters and also the economic weights are known without error. Only then will the calculated index yield maximum genetic improvement. In practice, however, these parameters are not known exactly and estimates are used instead. The net result of imperfect knowledge about the parameters is that the indexes actually calculated will yield progress somewhat less than the maximum attainable.

1. Genetic and phenotypic parameters

The reliability of the genetic and phenotypic parameters will depend on the estimation procedure, the structure of the data and the sample size. Harris (1961 and 1964) and Williams (1962a and 1962b) have pointed out the importance of using a considerable amount of data for index construction. Harris (1964) concluded that there is a tendency to overestimate the progress from selection for a particular calculated index. The considerable discrepancies with a limited amount of data become fairly small with a sufficient amount of data (suggested are at least 1,000 individuals). Further, the magnitude of the bias seems in general to be related inversely to the magnitude of the genetic gain. The work of Heidhues (1961) is in agreement with Harris (1961 and 1964), and suggests the full utilization of the genetic knowledge of the population structure. Following Heidhues (1961) the occasionally used practice of assuming the genotypic covariances between the traits to be zero, is not generally recommended. Recently Pease et al. (1967) have shown by a rather rough investigation that errors in the heritabilities do not seem

to upset the balance of an index as much as errors in some individual covariances. Underestimating the heritabilities by 0.1 lowered the efficiency of the index in no case by more than 0.6 percent. The effects of errors in the phenotypic and genotypic correlations are different from trait to trait, depending upon the magnitude of the correlations and the relationships with other traits. Pease et al. (1967) have shown that the efficiency of an index is more sensitive to errors in the phenotypic correlations than to errors in the genetic correlations. In the most sensitive case, an error of 0.3 in the correlation between feed efficiency and dissected lean cuts, resulted in about 6 percent loss in efficiency. Such a loss might not invalidate the index but is equivalent to a substantial waste of testing space. The effects of errors in phenotypic correlations appeared to be somewhat larger. In spite of this, genetic correlations are likely to be more of a problem since the errors of estimation are greater.

2. Economic weights

Relatively little research has been directed toward examining the problems and properties of economic weights. The estimation of economic weights is not very easy as will be pointed out later. Relative costs and prices may fluctuate periodically, or for some traits, the necessary data are not available. For these reasons the estimates of economic weights are often rather approximate. It is therefore important to know to what extent they influence the index and the efficiency of it. Pease et al. (1967) have made some considerations on the effect of errors in the economic weights. The economic weights were not found to be very critical.

Extreme errors of as much as 50 percent resulted in the worst case in a loss of relative efficiency of 1.8 percent. Recently Rønningen (1971b) studied the effect of false economic ratio's between two traits on the change in aggregate genotype for a two-trait index. The criterion used was the difference between the correlation of the correct aggregate genotype and the correct index, and the correlation of the correct aggregate genotype with a biased index (calculated with wrong aggregate genotype). Rønningen (1971b) concluded that the loss in efficiency is not too serious when moderate deviations from the true economic ratio are used. The loss increased as the deviation from the true economic ratio increased. When the economically most important trait was given a negative weight, the loss was substantial, especially when the heritability was high.

III. DATA AND METHODS OF PROCEDURE

To compare the efficiency of different selection indexes and to study the effect of errors in the economic weights, a set of selection indexes had to be developed. For this purpose a basic selection index was designed for a "Combined Testing" scheme for pigs. Four pigs from the same litter were to be tested, two boars in a performance test (in individual pens), and two full-sibs to obtain carcass information (in the same pen). The information contained in the complete index and the traits of the aggregate genotype are listed in Table 1.

A. Genetic and Phenotypic Parameters

Since the estimation of the necessary genetic and phenotypic parameters was a research project on its own, and was not the real purpose of this study, it was decided to collect data from the literature. We have to recognize that such a procedure is far from ideal. After carefully scrutinizing the literature, the most consistent figures were retained, and extreme values were removed. The heritability coefficients, and the genetic and phenotypic correlations are compiled in Table 2. The sources were Jonsson (1965), Fredeen (1953), Pease et al. (1967), Christian (1970), Vint (1971), Siers and Thomson (1972) and Sutherland (1958).

1. Calculation of variances and covariances

All variables were standardized by dividing each trait in the index by the corresponding phenotypic standard deviation of the boar. The

Table 1. Reference number and list of traits included in the variance covariance tables

Trait number	Description of trait
Index	
1.	Daily gain of boar 1
2.	Feed efficiency of boar 1
3.	Probe of boar 1
4.	Daily gain of boar 2
5.	Feed efficiency of boar 2
6.	Probe of boar 2
7.	Average (pen) feed efficiency of boar 1 and 2
8.	Average carcass backfat of barrow and gilt
9.	Average dressing percentage of barrow and gilt
10.	Average percent ham and loin of barrow and gilt
11.	Average loin-eye of barrow and gilt
12.	Average daily gain of barrow and gilt
13.	Average feed efficiency of barrow and gilt
14.	Number of pigs weaned
Aggregate genotype	
1'.	Daily gain
2'.	Feed efficiency
3'.	Carcass backfat
4'.	Dressing percentage
5'.	Percentage ham and loin
6'.	Loin-eye area
7'.	Number of pigs weaned

Table 2. Genetic correlations (top triangle) and phenotypic correlations (bottom triangle) and heritabilities

	1	2	3	4	5	6	7	8	h^2
1. Daily Gain		-0.68	0.20	0.15	-0.13	-0.20	-0.15	0.00	0.30
2. Feed eff.	-0.62		0.38	0.38	-0.15	-0.35	-0.13	0.00	0.35
3. B.F. Probe	0.15	0.35		1.00	0.15	-0.45	-0.13	0.00	0.45
4. B.F. Carcass	0.10	0.32	0.70		0.15	-0.40	-0.30	0.00	0.45
5. Dressing %	-0.10	-0.17	0.10	0.15		0.17	0.20	0.00	0.30
6. % ham + loin	-0.15	-0.35	-0.40	-0.45	0.10		0.60	0.00	0.45
7. Loin-eye	-0.10	-0.10	-0.20	-0.30	0.20	0.54		0.00	0.55
8. # weaned	0.00	0.00	0.00	0.00	0.00	0.00	0.00		0.10

standard deviations were multiplied by the economic weights to express the economic weights in standard deviation units. The variances and covariances were calculated with the following formulas:

Phenotypic variance: 1

Genetic variance for the boar: h^2

Phenotypic covariance between x and y both measured on the boar: r_p

Genetic covariance between x and y both measured on the boar: $h_x h_y r_g$

Phenotypic variance of the mean of n sibs: $\frac{1}{n}\left[1 + (n-1)(\frac{h_x^2}{2} + e_x^2)\right]$

Genetic variance of the mean of n sibs: $h^2(\frac{n+1}{2n})$

Phenotypic covariance between the mean variable x measured on n_1 sibs and y measured on n_2 sibs, with n_{12} sibs common to both groups:

$$\frac{1}{n_1 n_2}\left[n_{12} r_p + (n_1 n_2 - n_{12})(\frac{1}{2} h_x h_y r_g + e_x e_y r_e)\right]$$

Genetic covariance between the mean x measured on n_1 sibs and mean y measured on n_2 sibs with n_{12} sibs in common:

$$h_x h_y r_g\left[\frac{n_1 n_2 + n_{12}}{2 n_1 n_2}\right]$$

Phenotypic covariance between variable x measured on the boar and mean y measured on k sibs:

$$\frac{1}{2} h_x h_y r_g + e_x e_y r_e$$

Genetic covariance between variable x measured on the boar and mean y measured on k sibs: $\frac{1}{2} h_x h_y r_g$.

h_x^2 and h_y^2 are the heritabilities for traits x and y

r_p is the phenotypic correlation

r_g is the genetic correlation

e_x^2 and e_y^2 are the litter environment components of variance for traits x and y.

The litter environment component of variance (e^2) was 0.1 and the corresponding environmental correlations equal to the phenotypic correlations. The calculated phenotypic variances and covariances (P matrix) are given in Table 3. The genetic covariances between the traits in the index and the aggregate genotype (G matrix) are given in Table 4. And the genetic variances and covariances of the traits in the aggregate genotype (C matrix) are given in Table 5.

B. Economic Weights

Economic weights can be estimated following different procedures:

- short cut method (using the simple relationships of costs and prices between the economically important traits)
- multiple regression technique (economically important traits regressed on net profit)
- partial differentiation of a profit function (increments of change from the mean in the economically important traits)
- iterative procedure.

Table 3. The n x n P matrix of phenotypic variances and covariances

Trait	1	2	3	4	5	6	7
1	1.000	-0.620	0.150	0.250	-0.172	0.052	-0.396
2		1.000	0.350	-0.172	0.275	0.110	0.637
3			1.000	0.052	0.110	0.325	0.230
4				1.000	-0.620	0.150	-0.396
5					1.000	0.350	0.637
6						1.000	0.230
7							0.637
8							
9							
10							
11							
12							
13							
14							

8	9	10	11	12	13	14
0.037	-0.029	-0.052	-0.040	0.250	-0.172	0.000
0.107	-0.041	-0.104	-0.038	-0.172	0.275	0.000
0.295	0.037	-0.139	-0.052	0.052	0.110	0.000
0.037	-0.029	-0.052	-0.040	0.250	-0.172	0.000
0.107	-0.041	-0.104	-0.038	-0.172	0.275	0.000
0.295	0.037	-0.139	-0.052	0.052	0.110	0.000
0.107	-0.041	-0.104	-0.038	-0.172	0.275	0.000
0.662	0.098	-0.274	-0.187	0.068	0.197	0.000
	0.625	0.071	0.130	-0.059	-0.105	0.000
		0.662	0.343	-0.101	-0.209	0.000
			0.687	-0.070	-0.064	0.000
				0.625	-0.396	0.000
					0.637	0.000
						1.000

Table 4. The n x m G matrix of genetic variances and covariances

Trait	1'	2'	3'	4'	5'	6'	7'
1	0.300	-0.221	0.055	-0.039	-0.074	-0.061	0.000
2	-0.221	0.350	0.150	-0.048	-0.138	-0.057	0.000
3	0.074	0.150	0.449	0.055	-0.198	-0.149	0.000
4	0.150	-0.110	0.027	-0.019	-0.037	-0.030	0.000
5	-0.110	0.175	0.075	-0.024	-0.069	-0.028	0.000
6	0.037	0.075	0.225	0.027	-0.099	-0.074	0.000
7	0.165	0.262	0.112	-0.036	-0.103	-0.043	0.000
8	0.027	0.075	0.225	0.027	-0.099	-0.075	0.000
9	-0.019	-0.024	0.027	0.150	0.031	0.040	0.000
10	-0.037	-0.069	-0.099	0.031	0.225	0.148	0.000
11	-0.030	-0.028	-0.074	0.040	0.146	0.275	0.000
12	0.150	-0.110	0.027	-0.019	-0.037	-0.030	0.000
13	-0.110	0.175	0.075	-0.024	-0.069	-0.028	0.000
14	0.000	0.000	0.000	0.000	0.000	0.000	0.050

Table 5. The m x m C matrix of genetic variances and covariances

Trait	1'	2'	3'	4'	5'	6'	7'
1'	0.300	-0.221	0.055	-0.039	-0.074	-0.061	0.000
2'		0.350	0.150	-0.048	-0.138	-0.057	0.000
3'			0.450	0.055	-0.198	-0.149	0.000
4'				0.300	0.063	0.081	0.000
5'					0.450	0.297	0.000
6'						0.550	0.000
7'							0.100

It would be interesting to evaluate the merits of these methods. However, the necessary information for a multiple regression estimation is not available. A workable set of economic weights will be estimated by the so called "short cut" method, while the partial differentiation method and the iterative procedure will be discussed later.

1. Daily gain

There is a certain amount of controversy over the economic importance of daily gain. The reason is that there are three economic components involved and two of them only apply in certain circumstances. The first component is reduction in labor costs. James and Trede (1967) studied the records of 38 Iowa swine farms with respect to different production systems; some of their figures are given in Table 6. The over-all average labor requirement per hog produced (growing and finishing period) was 0.82 hours. Hence labor costs were $1.64 per hog if labor is calculated at $2.00 per hour. The differences among systems were of minor magnitude. A total weight gain of 200 pounds (from weaning to slaughter) at 1.96 pounds per day requires a feeding period of 102 days and an increase of the average daily gain of 0.10 reduces the feeding period by 4.9 days and the labor costs by $0.08.

The second component is overhead costs (depreciation, interests, taxes, insurance and repairs for buildings and equipment). This component can only be taken into account if one is working on a multiple farrowing basis and growing pigs at all times of the year. In a two-litter system we have to finish two pig crops and the overhead costs

Table 6. Average labor requirement per hog produced (feeding period) in hours (James and Trede, 1968)

	Multiple litter system				Two-litter system		
All farms	Tot. conf.	Part. conf.	Part. conf. + past.	WS[a] Part conf. + past.	WS[a] part. conf.	SF[b] part. conf. + past.	SF[b] part. conf.
0.82	0.80	0.78	0.71	0.82	0.65	0.87	0.92

[a]Winter and summer farrowing.

[b]Spring and fall farrowing.

Table 7. Average overhead cost per hog produced (feeding period) in dollars (James and Trede, 1967)

	Tot. conf.	Part. conf. drylot shelter	SF[a] part. conf.	WS[b] part. conf.	WS[b] part. conf. + past.
Growing - finishing building	3.70	3.19	1.86	1.86	1.86
Building equipment	4.43	1.89	1.31	1.31	1.42
Total	8.13	5.08	3.17	3.17	3.28

[a]Spring and fall farrowing.

[b]Winter and summer farrowing.

per pig are not affected by the average daily gain. For a multiple farrowing system (with nursing house) under total confinement, the overhead costs are approximately $5.00 per hog produced (Table 7) and for a two-litter system $3.20. Permitting a pen a rest period of 5 days (to clean, disinfect, etc...) a pig has a pen place for approximately 107 days. If we can reduce the feeding period by 4.9 days by increasing daily gain by 0.1 pound, the overhead costs per hog decrease by (4.9/107) x 5.00 = $0.23 per pig finished.

The third component consists of the potential increase of profit because of higher daily gain. In a continuous farrowing and finishing system, a higher daily gain makes it possible to finish an additional number of pigs which potential enables the farmer to increase profit for the same investment. In a continuous partial confinement system where average returns over total costs are $3.00 (based on a price of $18.00 per cwt., Table 8) the potential profit increase amounts to (4.9/107) x 3.00 = $0.14 per hog finished. When these three components are compiled for the two systems, we obtain the following figures:

Per hog produced for 0.1 increase in daily gain ($)	Continuous partial confinement	Two litters partial confinement
reduction in labor costs	0.08	0.08
reduction in overhead	0.23	-
potential profit increase	0.14	-
total	0.45	0.08

Table 8. Average returns per cwt based on constant price of $18 per cwt in dollars (James and Trede, 1968)

	All farms	Multiple litter systems			Two-litter systems			
		Tot. conf.	Part. conf.	Part. conf. + past.	WS[a] part. conf. + past.	WS[a] part. conf.	SF[b] part. conf. + past.	SF[b] part. conf.
Over variable costs	3.71	3.29	3.62	3.51	3.26	4.46	4.75	3.57
Over all costs	1.47	.23	1.37	1.36	1.44	2.12	2.30	1.43

[a]Winter and summer farrowing.

[b]Spring and fall farrowing.

The economic weights for daily gain are $0.45 per 0.1 pound for a continuous partial confinement system and $0.08 for a two-litter partial confinement system.

2. Feed efficiency

If the total weight gain from weaning to slaughter is 200 pounds and the cost of the feed is $2.90 per cwt then an improvement (decrease) of 0.1 pound feed per pound gain reduces the total feed consumption by 20 pounds and the total feed costs by $0.58.

3. Dressing %

For an empty pig of 205 pounds a 1% increase of the dressing percentage represents a yield increase of 2.05 pounds. If the average carcass is worth $30.00 per cwt[1] (USDA Economic Research Service, 1969), a 1% increase in dressing percentage has the value of $0.61.

4. Percent ham and loin

The value of the carcass can be divided in the value of ham and loin and the remainder

Ham + Loin	55.11 pounds a $0.4890[2]	=	$26.95
Remainder	101.92 pounds a $0.1977	=	$20.15
Total Carcass	157.03 pounds a $0.3000	=	$47.10

---

[1] $30.00 per cwt is the price for 1969 on a linear trend calculated for the period 1948-1969.

[2] These prices are trend values for 1969 from a linear trend calculated for period 1948-1969. The information has been compiled from the Livestock and Meat Statistics (USDA Economic Research Service, 1970).

If the amount ham and loin increases with 1.0 percent or with 1.57 pounds, the value of the carcass increases with 1.57 times the difference in price between the price of ham + loin and the rest. That is 1.57 (48.90 - 19.77) = $0.46.

5. Loin-eye area

Since loins with a very large loin-eye area and loins with a small loin-eye area are as likely to be lower priced than loins with an intermediate loin-eye area, it is very hard to estimate the relative economic value of this trait. Our estimate is based on the correlation between loin-eye area and percent lean cuts. We assume that for a given carcass (weight, length and percent ham and loin) increasing loin-eye area will result in (a) a direct increase in value of the loin (larger pork chops) and (b) indirectly, an increase of the percent ham and loin that will increase the value of the carcass. Since it is impossible to estimate (a) we will take the value of (b) as economic weight for loin-eye area. Arganosa et al. (1969) estimated the phenotypic correlation between loin-eye area and percent lean cuts at 0.49. Siers in 1966 found a phenotypic correlation between loin-eye area and percent loin and ham of 0.54. Using this last figure and assuming that this estimate is valid for the population with which we are working, the regression of loin-eye on percent ham and loin is 1.39. Thus a positive deviation (from the mean) of 1 sq. inch loin-eye results very roughly in a 1.39% increase of the percentage ham and loin. Since a 1% increase in ham and loin increases the value of the carcass by $0.46, a 1 sq. inch increase of the loin-eye area could be roughly estimated to be 1.39 x 0.46 = $0.63.

6. Carcass backfat

When carcasses are graded on carcass backfat alone, there is a price cut of approximately $0.50 per cwt for 0.30 inch carcass backfat or $1.88 per cwt per inch. This is $2.952 per inch for a 157-pound carcass.

7. Number weaned

Based on prices of feeder pigs (35-40 pounds) of $38 per 100 pounds or approximately $15.20 per pig, we can say that $15.20 is the additional gross return of weaning one more pig per litter (assuming no death loss between weaning and 35-40 pounds). If we only take the additional feed costs into account (44 pounds x 0.04 = $1.76) one additional pig is worth $13.24. If the average number weaned is 7.33 per litter and we have 3% death loss post weaning, we can sell 7.11 hogs per litter. The profit of 1 additional pig weaned per hog finished is then (13.2 /7.11) $1.86. The economic weights and the standardized economic weights are summarized in Table 9.

C. Calculated Indexes

The different calculated indexes are given in full detail in Appendix A. The subindexes (constituent indexes) of the main index are given in Appendix B. All index coefficients are in standardized form; for practical use, it might be desirable to transform such an index to an

Table 9. Summary of the economic weights in dollars

Triat	unit	ec. weight	stand dev.	ec. stand dev.
Daily gain continuous partial conf.	lb.	4.50	0.16	0.720
two-litter system	lb.	0.80	0.16	0.128
Feed efficiency	lb.	-5.80	0.25	-1.450
Carcass backfat	in.	-2.95	0.16	-0.472
Dressing percentage	%	0.61	1.65	1.006
Percent ham and loin	%	0.46	1.77	0.814
Loin-eye area	sq. in.	0.64	0.62	0.397
Number of pigs weaned	#	1.86	2.18	4.055

index with given mean and variance. The main index puts a lot of weight on feed efficiency. This is due to a favorable variance covariance structure and its relative economic importance. The total genetic gain breaks down as follows: 44.93 percent of total gain is accounted for by gain in feed efficiency, 18.23 percent in percent ham and loin, 10.54 percent in backfat, 9.23 percent in daily gain, 7.05 percent in dressing percent, 6.50 percent in loin-eye and 3.48 percent in average number weaned. Hence about 54.17 percent of the gain is realized in daily gain and feed efficiency, 42.34 percent in the carcass traits and 3.48 percent in reproductive efficiency. The strong negative weights on daily gain were unexpected. Further investigation showed that the negative weight for daily gain mainly came from the part of the index which was directed towards leanness. But, the effect of a negative index coefficient is more than offset by the correlated response from improving other traits, particularly feed efficiency. When the selection differential (SD) equals σI, the complete index improves daily gain with a value of $0.1004 per generation. When daily gain is deleted from the index, the indirect improvement in daily gain is $0.1067. If feed efficiency is deleted from the index, the b coefficient of daily gain becomes positive. The values of the variates in the complete index indicate that when direct information is available on the boar, additional information contributes only a little to the correlation of the index with the aggregate genotype. This will later be discussed in greater detail. The index coefficients of the different indexes are summarized with the relative efficiencies in Table 10.

Table 10. Different selection indexes and their relative efficiency

Trait number	Index number					
	1	2	3	4	5	6
1	-.1400	-.1400	.0775	-.1494	-.1494	-.1120
2	-.8168	-.8168	-	-.8256	-.8256	-.8380
3	-.1637	-.1637	-.3130	-.1576	-.1576	-.1586
4	-.0241	-.0241	-.2383	-.0336	-.0336	.0039
5	-.1589	-.1589	-	-.1677	-.1677	-.1801
6	-.0144	-.0144	.1329	-.0083	-.0083	-.0093
7	-	-	-.9710	-	-	-
8	-.0359	-.0359	-.0354	.0400	.0400	-.0425
9	.1934	.1934	.1936	-	-	.1912
10	.2357	.2357	.2360	.2064	.2064	.2333
11	.2383	.2383	.2389	.2876	.2876	.2294
12	.1668	.1668	.1662	.0647	.0647	-
13	-.0661	-.0661	-.0673	-.1892	-.1892	-
14	.2027	-	.2027	.2027	-	.2027
σ_I	1.0867	1.0676	1.0529	1.0788	1.0596	1.0757
R(IH)	.4908	.4822	.4755	.4872	.4785	.4858
Rel. eff.	100.00	98.24	96.88	99.26	97.49	98.98

Table 10. Continued

Trait number	Index number					
	7	8	9	10	11	12
1	-.1890	-.1890	-.1734	.4167	-	-.2351
2	-.9227	-.9227	-.8492	-	-.7135	-.9323
3	-.1551	-.1551	-.1469	-.5334	-.2162	-
4	-.0731	-.0731	-.0575	.1008	-	-.0415
5	-.2648	-.2648	-.1913	-	-.1430	-.1769
6	-.0058	-.0058	.0024	-.0875	-.0190	-
7	-	-	-	-	-	-
8	-	-	-	-.0272	.0117	-
9	-	-	-	.3222	.1675	.1492
10	-	-	-	.3872	.2027	.2368
11	-	-	-	.2184	.2559	.2470
12	-	-	-.1131	.2749	-	.1228
13	-	-	-.3803	-	-.1952	-.1142
14	.2027	-	.2027	.2027	.2027	.2027
σ_I	1.0053	.9846	1.0317	.9393	1.0808	1.0773
R(IH)	.4540	.4447	.4660	.4242	.4881	.4866
Rel. eff.	92.50	90.60	94.94	86.43	99.44	99.14
	147.38[a]	144.35[a]				

[a]Relative efficiency corrected for increase in selection intensity (when fraction saved dropped from 50 to 25%).

Table 10. Continued

Trait number	Index number				
	13	14	15	16	17
1	-.2308	-.1378	-.1491	-.1442	-.1654
2	-.9279	-.8139	-.8254	-.8223	-.8434
3	-	-.1698	-.1607	-.1545	-.1417
4	-.0371	-.0219	-.0332	-.0283	-.0495
5	-.1725	-.1560	-.1675	-.1644	-.1855
6	-	-.0206	-.0114	-.0052	.0076
7	-	-	-	-	-
8	-.0971	-	-.0495	-.0949	-.1667
9	.1847	.1824	.1668	.2543	.2488
10	.2311	.2379	-	.3638	-
11	.2282	.2456	.3318	-	-
12	.1711	.1507	.0532	.2227	.0429
13	-.0535	-.0868	-.2034	.0143	-.1932
14	.2027	.2027	.2027	.2027	.2027
σ_I	1.0791	1.1804	1.0780	1.0745	1.0476
R(IH)	.4874	.4907	.4868	.4843	.4731
Rel. eff.	99.30	99.97	99.18	98.67	96.37

IV. RESULTS AND DISCUSSION

A. Value of Additional Information in a Selection Index

A selection index for practical use should meet the following requirements:

1) The aggregate genotype should contain only economically important traits.
2) An index should contain all the information necessary to maximize the genetic change in the aggregate genotype with the restriction that for each piece of information in the index, the cost of including this information is less than the discounted returns (increased ΔH).

In this discussion we shall restrict our attention to the second requirement and try to answer the following questions:

- What is the economic value of carcass information from sibs in a boar performance testing scheme?
- What is the economic value of pen-feed efficiency versus individual feed efficiency?
- What is the economic value of additional information on the sibs (i.e. daily gain and feed efficiency) in a boar performance testing scheme?

The basic index information and the relative efficiency of the various indexes is compiled in Table 10.

1. Evaluation of costs and returns

When the average selection intensity $\bar{i}$ and the generation interval t

are given, the overall genetic gain per generation obtained with the complete index can be calculated with formula (14). The percentage reduction in efficiency is given by formula (46), so that we can estimate the effect (in dollars) on the genetic gain of deleting a piece of information from the index.

If C is the cost of obtaining the information per boar tested and p is the fraction of boars selected, C/p is the cost of obtaining the information per selected boar. C/p can be considered as an investment in year y_o that will end delivering returns in year y_N, when the last progeny is commercialized. The cost per boar selected in year y_o is:

$$Cy_o = C/p \tag{47}$$

If we assume that the selected boars are only used in commercial herds and that random mating is practiced, the additional return to the progeny in year y_o--because of selection using an index with additional information--is the expected discounted accumulated return of selling superior (commercial) progeny. The discounted accumulated return per selected boar is given by:

$$AR = R \sum_{k=2}^{N} r_k (1 + i)^{-y_k} \tag{48}$$

where

R is the additional return per pig because of selection using additional information

r_k is the number of commercializable progeny in year k

i is the interest rate per year

y_k is the time in years between the test and first commercialization of progeny (k=2) and the last (k=N).

Only a minor error will be made if we define r as the average number of commercializable progeny a boar produces per year. Expression (48) then becomes:

$$AR = rR \sum_{k=2}^{N} (1 + i)^{-y_k} \tag{49}$$

By setting $Cy_o = AR$ we can calculate the average number of progeny required to equal the cost of additional information:

$$r^* = \frac{C/p}{R \sum_{k=2}^{N} (1 + i)^{-y_k}} \tag{50}$$

Then the profit expressed per boar selected from investing in additional information in year y_o is:

$$P = (n - r^*)R \sum_{k=2}^{N} (1 + i)^{-y_k} \tag{51}$$

where n is the normal number of progeny per boar. In year y_o, the total return from testing M and selecting Mp boars would be:

$$AR_m = npMR \sum_{k=2}^{N} (1 + i)^{-y_k} \tag{52}$$

where AR_m is the expected discounted return from testing M boars. Then the net profit from selection on the basis of additional information is:

$$P_m = pMnR \sum_{k=2}^{N} (1 + i)^{-y_k} - pMC/p \quad . \tag{53}$$

The profit per boar tested is:

$$P_m/M = pnR \sum_{k=2}^{N} (1 + i)^{-y_k} - C \qquad (54)$$

2. Multiplier herds

From relationship (54) it can be seen that the profit per boar tested will increase if n (the normal attainable reproductive rate) increases. With that respect we have two options. The selected boars can be used immediately in commercial herds (open system). The total genetic gain after y generations of selection will be:

$$(\Delta H)_y = k \bar{i} R(HI)\sigma H y \qquad (55)$$

where k is the ratio of boars which are actually selected from the test over the total number of boars used in the population; or, via a system of elite and multiplier herds, to use only the offspring from the selected boars in commercial herds. The elite herds have then the monopoly of the testing facilities. They produce all the tested boars for themselves and for the multiplier herds. This system often called "closed system" has the advantage that the number of multiplier herds can be chosen such that all the boars used in these herds can be tested or that the selection intensity can be increased. A sufficient large number of F_1 boars can then go to commercial herds. The same idea is used by the breeding industry to spread the research and development costs of their commercial product. C. Smith (1958) pointed out that the genetic gain in the multiplier herds after y generations of selection in the nucleus

is approximately:

$$(\Delta H)_y = k'\bar{I}R(HI)\sigma H\ (y - 2) \qquad (56)$$

k' is the fraction of tested boars used in the multiplier herds and is usually equal to one. The genetic gain in the commercial herds is (Bichard, 1971):

$$(\Delta H)_y = k''\bar{I}R(HI)\sigma H\ (y - 4) \qquad (57)$$

k'' is the fraction of F_1 boars (from the multiplier herds) used in the commercial herds. Thus progress in the commercial herds begins four generations after the boars were selected in the elite herds. This means a delay of two generations compared with the open system. The discount factor will be greater, but n and also k'' will be much greater.

3. Open system

According to C. Smith (1969) the optimum fraction selected, when not all the boars in the population can be tested is 0.50. In the case where no sib information is used the testing capacity can be doubled and the fraction saved can be reduced to 0.25. We are assuming a generation interval of 2.2 years and that no selection is practiced on females. A boar is in service from 8 months of age until he becomes three years old. We assume 25 sows per boar, an average of 1.7 litters per sow per year and 7 pigs per litter.

The cost of obtaining the additional information was calculated as follows:

(a) carcass information on sibs: $3.00 per slaughtered litter mate

or per boar tested.

(b) sib information. The system of two individually fed boars and two sibs was converted to a system in which four boars could be individually fed (two times two litter mates). Labor was calculated at $2.00 per hour. The balance of savings and expenses was as follows:

	Savings	Expenses
- carcass information	6.000	
- remodeling pen (depreciation, interest and insurance on watercup, feeder and pen separation)		4.125
- additional probing costs		0.120
- additional feeding costs		3.420
	6.000	7.665

This is a real cost of $1.665, or $0.416 per boar tested.

(c) daily gain and feed efficiency on sibs. The cost of weighing and recording was estimated at half of the total feeding and recording costs or $0.855 per boar tested.

(d) individual feed efficiency of boars versus pen feed efficiency. The remodeling costs of the pen and the additional feeding and recording costs were estimated at $3.722 per boar tested.

Interest rates were 6% and the commercialization of the boar progeny started the first year after testing and ended in the third year, thus N is equal to four. The estimated profit, according to the previous developed formulas for the open system, is given in Table 11.

Table 11. The economic value of additional information in a selection index

	Carcass inform. on sibs	All sib inform.	D. gain and feed eff. on sibs	Pen feed eff. instead of individual feed eff.
a) open system				
- loss in relat. eff. if information is deleted and selection intensity is constant (%)	5.05	7.50	1.02	3.12
- % saved (p)	0.50	0.25	0.50	0.50
- average sel. intensity if no selection on females (i)	0.3989	0.6357	0.3989	0.3989
- ΔH full index ($/generation)	0.433496	0.433496	0.433496	0.433496
- ΔH reduced index ($/generation)	0.411591	0.639034	0.429079	0.425255
- reduction in ΔH ($/generation)	0.021905	-0.205538	0.004417	0.008241
- cost of additional infor. per boar tested ($):C	3.000	0.416	0.855	3.772

Table 11. Continued

	Carcass inform. on sibs	All sib inform.	D. gain and feed eff. on sibs	Pen feed eff. instead of individual feed eff.
- cost of additional infor. per boar selected ($):C/p	6.000	1.664	1.610	7.544
- number commercial offspring in career of boar	694.07	694.07	694.07	694.07
- average number commercial offspring per year (F_1):n	231.8	231.8	231.8	231.8
- average number commercial offspring needed per year to break even: r*	102.5	-	136.4	342.5
- profit per boar tested ($):$P_m/M$	3.40	-30.45	0.43	-1.36
b) <u>closed system</u>				
- average number F_2 offspring per year: $_2$n*	12,738.8	12,738.8	12,738.8	12.738.8
- profit per boar tested ($): P_m/M	473.62	-2,236.54	95.25	175.55

4. Closed system

The basic assumptions are the same as with the open system. The additional assumptions are that the multiplier herds can sell an average of two boars per litter to the commercial herds. Thus the rate is 65.16 multiplier boars per selected boar per year, or 195.50 boars in the lifetime of a tested boar. Each of the F_1 boars can again give 694.07 F_2 progeny. We assume no selection on females and no selection in the multiplier herds. For this system we can adapt formula (54) as follows:

$$P_m/M = pnR \sum_{k=2}^{N} (1+i)^{-y_k} + pn^*R' \sum_{k=3}^{N+1} (1+i)^{-y_k} + \qquad (58)$$

(1) (2)

$$pn^*R' \sum_{k=4}^{N+2} (1+i)^{-y_k} + pn^*R' \sum_{k=5}^{N+3} (1+i)^{-y_k} - C$$

(3) (4)

Where R' is $R/2$ since the boars only transmit half of their superiority on their offspring and there is no selection on females

n^* is the average number of progeny from F_1 boars per tested boar per year. This is equal to the average number of F_1 boars (that is produced in multiplier herds and sold to commercial herds) per year per boar selected (65.16), multiplied by the average number progeny per boar per year (231.38).

(1) is the return realized in the multiplier herd from the commercialization of the (F_1) progeny from the initial tested boar

(2) is the return realized in the commercial herds from the first year (F_2) progeny from the F_1 boars.

(3) is the return realized in the commercial herds from the second year (F_2) progeny from the F_1 boars.

(4) is the return realized in the commercial herds from the third year (F_2) progeny from the F_1 boars.

Formula 58 can be simplified to:

$$Pm/M = pR \left[n \sum_{k=2}^{N} (1 + i)^{-y_k} + \frac{1}{2} n^* \sum_{j=1}^{3} \sum_{k=2+j}^{N+j} (1 + i)^{-y_k} \right] - C .$$

The estimate of profit for a closed system is given in Table 11.

5. Discussion

The estimates in Table 11 (open system) strengthen the already existing belief that carcass information on sibs pays off only when it does not affect the selection intensity. If because of taking carcass information on sibs, we decrease the selection intensity from 1.2729 to 0.7979 as in our example carcass information on sibs will from an economic point of view, never be justified. The potential loss is $30.45 per boar tested.

The additional profit from daily gain and feed efficiency of sibs (assuming that we already are feeding two sibs to obtain carcass information) is only $0.43 per boar tested. Individual feed efficiency of the boars as compared with pen feed efficiency is not justified under the assumptions made here. The loss per boar tested is $1.36.

The values in Table 11 (closed system) illustrate the amplification

power of a multiplier system. While in the open system individual feed efficiency of the boars was not profitable it gives $175.55 profit in a closed system. These estimates will largely depend upon the assumptions made. A ΔH realized in one generation will in a closed population be carried through in all subsequent generations. Since we only took the commercial value of the pig into account and ignored the effect of an initial selection upon the coming generations, our estimate of profit will be rather conservative.

6. Economic risk from genetic uncertainties

In practice, the expected gain from selection indexes is predicted from genetic and phenotypic estimates of parameters and from relative economic weights. It has been shown (Harris, 1964) that when the genetic parameters are subject to rather high standard errors, selection indexes with estimated parameters tend to over-estimate the "true" genetic gain. This, however, should be less serious when the estimates are based on a large number of observations. Genetic gain from selection can also be attenuated by "genetic slippage" in the population (Dickerson, 1955). This may result from limited population size, heterozygote superiority of fitness and recurrent loss of favorable epistatic combinations from one generation to the next. In view of the genetic uncertainties that might affect a population, the evaluation of the potential economic value of information in a selection index is encircled by a degree of speculation.

B. Some Suggested Indexes

The calculated indexes given in Appendix B and in Table 10 are in standardized form. It is not the primary purpose of this study to construct selection indexes. However, since this information can so eaily be made available, some of the more practical indexes will be presented in this section. For this purpose we transformed the indexes of Table 10 to destandardized indexes with a standard deviation of 33.33 points and a mean of 100.00. The measurements (variables) are expressed as deviations from the mean. The results are listed in Table 12.

Preliminary research at Iowa State University (L. L. Christian, 1972. Personal communication) indicates that ultrasonic measurements of the loin-eye area on live pigs are reasonable accurate. Therefore we have also calculated some indexes that include ultrasonic loin-eye measurements assuming the same phenotypic and genetic parameters as for the loin-eye area measured on the carcass.

The results indicate that measuring pen feed efficiency of the boars decreases the relative efficiency as compared with the complete index (index nr. 1) by approximately 3%. Deleting the information of the second (full sib) boar reduces the relative efficiency by approximately 2%, while the carcass information on two sibs accounts for about 9%. Under the assumptions made, ultrasonic measurement of loin-eye area on the boar improves the relative efficiency by approximately 12%, which means that an index without any sib information but with ultrasonic loin-eye measurement should be approximately 3% more efficient than an index with complete

Table 12. Some useful, destandardized and transformed indexes

Trait number	Index number[a]		
	1	3	8
Constant	100.00	100.00	100.00
1. Daily gain boar 1	-26.83	15.35	-39.98
2. Feed eff. boar 1	-100.21		-195.21
3. Probe boar 1	-31.37	-61.93	-32.80
4. U.S. loin-eye boar 1			
5. Daily gain boar 2	-4.61	-47.15	-15.46
6. Feed eff. boar 2	-19.49		-35.85
7. Probe boar 2	-2.75	26.30	-1.21
8. U.S. loin-eye boar 2			
9. Pen feed eff. boars		-122.95	
10. Av. carcass backfat sibs	-6.88	-7.00	
11. Av. dressing pct. sibs	3.59	3.71	
12. Av. pct. ham & loin sibs	4.08	4.22	
13. Av. loin-eye sibs	11.81	12.20	
14. Av. daily gain sibs	31.97	32.89	
15. Av. feed eff. sibs	-8.11	-8.52	
16. Av. number weaned	2.88	2.97	
R(IH)	0.4908	0.4755	0.4447
Rel. eff.	100.00	96.88	90.60
Rel. eff. adjusted[b]			144.53

[a]The index numbers correspond with the indexes given in Appendix B.

[b]Adjusted for increased selection intensity.

Table 12. Continued

Trait number	Index number[a]					
	18	19	20	21	22	23
Constant	100.00	100.00	100.00	100.00	100.00	100.00
1.	-10.76	-11.47	-27.79	-11.43	19.04	3.97
2.	-155.69		-214.20	-108.58		
3.	-12.01	-78.14	23.03	-21.19	-51.11	-66.92
4.	24.37			26.19	28.06	
5.	-0.47					-63.27
6.	-3.99					
7.	24.36					31.17
8.	3.15					
9.		-131.80			-104.09	-166.66
10.						
11.						
12.						
13.						
14.						
15.						
16.						
R(IH)	0.5018	0.4144	0.4334	0.4917	0.4812	0.4277
Rel. eff.	102.24	84.43	88.30	100.18	98.04	87.14
Rel. eff. adjusted)[b]	163.10	134.69	140.86	159.81	156.40	139.01

Table 12. Continued

Trait number	Index number[a]				
	24	25	26	27	28
Constant	100.00	100.00	100.00	100.00	100.00
1.	13.93	17.74	20.46	-17.87	13.41
2.				-165.83	-176.03
3.	-45.20	-71.83	-70.30	-21.22	-20.37
4.	25.91				
5.	-43.79				
6.					
7.	21.29				
8.	2.36				
9.	-128.80	-95.70	-104.70		
10.		1.87	-1.71	-9.16	-13.21
11.		4.18	4.39	3.73	3.94
12.		4.67	4.92	4.27	4.53
13.		13.11	12.49	12.07	11.38
14.		21.48		32.31	
15.		-13.87		-14.60	
16.					
R(I,H)	0.4849	0.4586	0.4544	0.4780	0.4704
Rel. eff.	98.79	93.43	92.58	97.39	95.84
Rel. eff. adjusted[b]	157.59				

(carcass) information on two sibs. This would not only allow us to test twice as many boars and increase the selection intensity (reducing the fraction saved (b) from 50 to 25% increases the selection differential by 59.33%) but also provide a slightly more efficient index. However, more data and the appropriate genetic and phenotypic parameters are needed to make a complete evaluation of ultrasonic loin-eye measurements.

Even without ultrasonic loin-eye measurements, the results in Table 12 indicate that indexes without any carcass information on sibs are at least 34% more efficient than indexes with carcass information on sibs. The acceptability of a pure performance testing procedure will depend on the educational value that the pork industry is willing to attribute to carcass information. Increasing problems with Porcine Stress Syndrome and meat quality might play a decisive role in this choice because the carcass information on sibs will be more valuable than assumed here. Unless this situation develops, the use of sibs to provide carcass information does not yield sufficiently valuable additional information to offset the decrease in selection intensity.

C. The Effect of Errors in the Economic Weights

1. Introduction

The selection index theory assumes that the economic weights are known fixed constants. For various reasons this assumption is almost never fulfilled.

a. Economic weights are estimates In the most favorable case, when we have complete information, multiple regression technique can be

used to determine the economic weights. In this case the economic weights are unbiased, but have usually fairly large sampling errors. For some traits, however, (i.e., loin-eye area and color score) the economic information is lacking or only partially available. In these circumstances economic weights are really no more than intelligent guesses rather than accurate estimates.

b. Fractionated structure of the industry The industry is made up of many breeders, commercial producers, and packers. Every individual has his own ideas and goals, and each tends to work in the economic framework of his own enterprise. For this reason every breeder and producer has his own set of economic weights. Because of the long-term nature of a breeding policy, the industry as a whole should have a well-defined set of realistic goals from which rather minor, but not major deviations are justified.

c. Time dimension Economic weights reflect production cost and consumer preference through the pricing mechanism. They are affected by price trends of feed grains, labor, construction costs, the qualitative and quantitative trends in the demand for pork meat and its substitutes and by technical innovations. Therefore the economic weights have to be adjusted periodically for changing economic situations and selection goals.

d. Improvement lag The dissemination of additive genetic improvement through a multiple tier breeding structure (nucleus, multiplier and commercial herds) requires time. The extent to which each tier is genetically behind the previous one, has been termed the "improvement

lag." These lags are considerable and the size is determined by the annual rate of progress in the nucleus, the age structure of the different tiers and the degree of genetic gain achieved in each tier. In order to use the proper economic weights in conformance with consumer preference and state of technology at time t_o, we should use projected economic weights for time $(t_o + \Delta t)$ where Δt is the total time lag between the genetic improvement in the nucleus herd and its appearance in the commercial herds. It has been shown by Bichard (1971) that the lag in improvement for a pig breeding structure varies from 7.5 years for a 3 tier pedigree selection system to 3.25 years for a performance testing scheme in which performance tested AI boars are used in commercial herds.

Since long term projections of price relationships and economic conditions in general are likely to have poor accuracy, frequent re-evaluation of economic weights is indicated. Even then, sampling errors may influence the estimates actually chosen to establish breeding goals.

This makes it evident that the "fixed constant" concept of economic weights is only relative. The important consequences of this are that by using a biased set of economic weights or by delaying the proper adjustments, the accuracy of selection will be reduced. In this section we will confine ourselves to the effect of variation and errors in the economic weights on index selection.

2. Concepts

A basic knowledge of how the genetic gain and the efficiency of a selection index is affected when the economic weights are biased and of how the relative efficiency or loss in relative efficiency will be

measured is important for the understanding of the following sections. The gain in the aggregate genotype (ΔH) can be represented by

$$\sum_{i=1}^{m} a_i \Delta G_i$$

or in a matrix notation by

$$\Delta H = a' \Delta G \tag{59}$$

where a' is a 1 x m vector of economic weights and ΔG is a m x 1 vector of gains in the individual traits ($\Delta G_i = R(IG_i)\sigma G_i i$) in metric units. Expression (59) has the nice property of exhibiting what happens to ΔH when the economic weights are biased. Assuming that all phenotypic and genetic parameters are known, we will denote ΔH, a and ΔG as the gain in the aggregate genotype, the economic weight vector and the vector of genetic gains in the individual traits when the economic weights are known without error. $\hat{\Delta H}$, $\hat{a}$ and $\hat{\Delta G}$ are the corresponding parameters when the economic weights are biased. We can express $\hat{\Delta G}$ and $\hat{a}$ by

$$\hat{\Delta G} = \Delta G + (\hat{\Delta G} - \Delta G)$$

$$\hat{a} = a + (\hat{a} - a)$$

and multiplication results in the following identities

$$\hat{a}'\hat{\Delta G} = a'\Delta G + (\hat{a} - a)'\Delta G + a'(\hat{\Delta G} - \Delta G) + (\hat{a} - a)'(\hat{\Delta G} - \Delta G) \tag{60a}$$

$$\hat{a}'\hat{\Delta G} = a'\Delta G + (\hat{a} - a)'\hat{\Delta G} \tag{60b}$$

Expression (60b) clearly indicates that errors in economic weights affect the estimated genetic gain in two different ways:

(a) Indirectly, because the ΔG vector is biased since ΔG_i is a

linear function of $R(IG_I)$. This is the effect of biases in the economic weights on the genetic gain in the individual traits expressed in metric units.

(b) Directly, because the second term of expression (60b) is multiplied by the vector of biases $(\hat{a} - a)'$ of economic weights.

Three different estimates of genetic gain can be considered:

ΔH is the expected genetic gain in the unbiased aggregate genotype H that results from selection on the corresponding unbiased index I.

$\Delta H|\hat{I}$ is the realized genetic gain in the unbiased genotype when selection is practiced on a biased index (calculated with biased economic weights).

$$\Delta H|\hat{I} = b(H\hat{I})\Delta\hat{I} = \frac{Cov(H\hat{I})}{\sigma\hat{I}}\, i$$

where $b(H\hat{I})$ is the regression of the unbiased aggregate genotype on the biased index and $\Delta\hat{I}$ is the selection differential.

$\Delta\hat{H}$ is the estimated genetic gain in the biased aggregate genotype resulting from selection on the corresponding biased index.

The relative efficiency of a selection index with respect to errors in the economic weights is

$$RE = \frac{R(H\hat{I})}{R(HI)}\ 100 = \frac{Cov(H\hat{I})}{\sigma\hat{I}\sigma I}\ 100 \qquad (61)$$

where $R(H\hat{I})$ is the correlation between the unbiased aggregate genotype with the biased index, and $R(HI)$ is the correlation between the unbiased aggregate genotype and the unbiased index. The loss in relative efficiency due to errors in the economic weights is

$$LRE = (1 - \frac{R(H\hat{I})}{R(HI)})100 \quad . \tag{62}$$

3. Errors in single economic weights

Effect on index coefficients The effect of a marginal change in the economic weights on the index coefficients (b vector) can be seen by taking the differential of b with respect to a (vector of economic weights).

$$\frac{\partial b}{\partial a} = \frac{\partial P^{-1}Ga}{\partial a} = P^{-1}G \quad .$$

In words, the effect on the i^{th} index coefficient of a change k in the j^{th} economic weight equals k(ij^{th} element of $P^{-1}G$). However, it can be more interesting to look at the relative changes in the b vector. This can be realized by dividing vector b by the total of its elements (T). The differential becomes:

$$\frac{\partial \frac{b}{T}}{\partial a} = \frac{T\frac{\partial b}{\partial a} - b\frac{\partial T}{\partial a}}{T^2} \tag{63}$$

where

$$\frac{\partial T}{\partial a} = \sum_{i=1}^{n} \frac{\partial b_i}{\partial a}$$

Since $\frac{\partial b_i}{\partial a}$ is clearly the i^{th} row of matrix $P^{-1}G$, after addition of all

$\frac{\partial b_i}{\partial a}$ elements we obtain a row vector that consists of the sums of columns of the $P^{-1}G$ matrix. Thus

$$\frac{\partial \frac{b}{T}}{\partial a} = \frac{1}{T}\{ P^{-1}G - \frac{b}{T} (\text{vector of column sums of } P^{-1}G)\} = DB .$$

This represents the relative effect on the i^{th} element of $\frac{b}{T}$ of a change δ_j in the j^{th} economic weight, which is approximately equal to δ_j(ij^{th} element of DB) for δ_j very small. A DA matrix has been calculated for the complete index and is given in Table 13. The values are scaled to give changes in $\frac{b}{T}$, i.e., changes in each weight as a percent of the sum of weights.

Example: If the true economic weight for daily gain was \$0.820 instead of \$0.720, then the weight given to feed efficiency of boar 1 should be -0.8168 + 10 x (0.0101) = -0.7158 approximately.

The DA matrix shows the most critical economic weights. However, the elements of the second differential of $\frac{b}{T}$ with respect to the economic weights are nonzero. This means that the effects of single changes are not linear and that the effects of multiple changes are nonadditive. For this reason the DB matrix is not really suitable to correct the index coefficients when the changes in the economic weights are large.

a. Effect on estimated genetic gain ($\Delta\hat{H}$) The change in $\Delta\hat{H}$ for a marginal change in the economic weights can be evaluated by differentiation with respect to the economic weight vector. Since

$$\Delta\hat{H} = \sigma i = (a'G'P^{-1}Ga)^{1/2}$$

Table 13. DB matrix: differentials of the vector b for the complete index with respect to the economic weight vector (x 10^{-2})

	1'	2'	3'	4'	5'	6'	7'
Trait							
1	-0.35	0.46	0.53	0.45	0.45	0.40	0.05
2	1.01	1.54	2.64	0.47	0.63	1.61	0.28
3	-0.05	0.35	-0.56	-0.39	0.24	0.61	0.06
4	-0.09	0.07	0.11	0.10	0.09	0.04	0.01
5	0.18	0.29	0.53	0.11	0.12	0.27	0.05
6	-0.01	0.04	-0.13	-0.07	0.02	0.11	0.00
8	0.01	0.06	-0.24	0.08	-0.12	-0.15	0.01
9	-0.09	-0.52	-0.59	-0.56	-0.02	-0.28	0.07
10	-0.11	-0.62	-0.78	-0.02	-0.80	-0.47	-0.08
11	-0.21	-0.64	-0.61	0.02	-0.21	-1.50	-0.08
12	-0.32	-0.41	-0.49	-0.07	-0.19	-0.36	-0.06
13	0.21	-0.07	0.22	-0.13	-0.19	0.10	0.02
14	-0.18	-0.56	-0.63	0.01	-0.04	-0.37	-0.20

(assuming a selection differential SD = σI)

$$\frac{\partial \sigma I}{\partial a} = \frac{1}{2} (a'GP^{-1}Ga)^{1/2} 2 (G'P^{-1}Ga) = \sigma I Ua \qquad (64)$$

where $U = G'P^{-1}G$

σI = a known scalar

Ua = a column vector consisting of the following elements $\sum_{i=1}^{n} U_{ij} a_i$.

It is easy to recognize that

$$\frac{\partial^2 f}{(\partial a)^2} \text{ and } \frac{\partial^2 f}{\partial a_i \partial a_j \; i \neq j} \neq 0$$

which merely tells that the effects of changes in the economic weights are neither linear nor additive.

The $\frac{\partial \sigma I}{\partial a}$ values for the complete index are listed below in dollars.

trait	$\frac{\partial \sigma I}{\partial a_i}$
1	0.1394
2	-0.3368
3	-0.2428
4	0.0763
5	0.2435
6	0.1781
7	0.0093

Example: If the true economic weight for feed efficiency were \$-1.250 instead of \$-1.450, the genetic gain would be 1.0867 + (0.200 x -0.3368) = 1.0194 approximately, instead of 1.0867.

To have a more realistic picture of the effect of errors in individual economic weights, errors ranging from minus 200 percent tc plus 200 percent were introduced in each economic weight separately. The results are given in Table 14. The effect on estimated genetic gain is plotted in Figure 1. These figures indicate that errors in the economic weights can result in relatively important under (negative errors) and over estimation (positive errors) of the genetic gain. For errors of minus 50 percent, the bias in estimated genetic gain ranges from minus 1.33 percent for number weaned to minus 22.91 percent for feed efficiency. For positive errors of 50 percent, the bias ranges from plus 2.15 percent for number weaned to plus 27.82 percent for feed efficiency. The magnitude of the bias is a function of the value of the affected economic weight, the heritability of the corresponding trait and the covariance structure of that trait with the other traits.

b. Effect on real genetic gain ($\Delta H|\hat{I}$) The effects of errors ranging from minus 200 percent to plus 200 percent in single economic weights on the real genetic gain are given in Table 14 and plotted in Figure 2.

Errors ranging from minus 50 percent to plus 50 percent have relatively little effect on the real genetic gain. Over this range, the reduction in real genetic gain is in all cases less than 1 percent.

This is also reflected by the loss in relative efficiency (LRE). The loss in relative efficiency due to errors in the economic weights ranging from minus 200 percent to plus 200 percent is given in Table 14 and plotted in Figure 3. The results indicate that:

- the loss in relative efficiency of a selection index due to errors in single economic weights is not symmetrical.
- negative errors (under-estimation of economic weights) are more critical than positive errors (over-estimation of economic weights).
- for errors between minus and plus 50 percent, the loss in relative efficiency varies between 0.16 percent and 0.90 percent.
- for larger errors (beyond the plus and minus 50 percent interval) can result in losses up to 10.14 percent and 76.44 percent for errors of minus 200 percent in the economic weights of daily gain and feed efficiency respectively.

It is of interest to know how the genetic gain in each individual trait is affected by errors in the economic weights. Since the genetic gain in trait j is a linear function of $R(IG_j)$ (the correlation of index and breeding value of trait j), the behavior of $R(IG_j)$ is a good indicator. The $R(IG_j)$'s were calculated with errors in each economic weight ranging from minus 200 percent to plus 200 percent. The results are listed in Table 15 and plotted in Figures 3 to 10. For relatively small errors (within a minus and plus 10 percent range) the correlations are relatively stable. The correlation of the index with the trait when its economic weight is directly affected shows more variation than the correlation with the indirectly affected traits. The economic weights for feed efficiency and daily gain are the most critical because both traits are highly correlated and have high relative economic weights.

The graphs also illustrate how by altering the economic weight of

Table 14. Estimated genetic gain, real genetic gain and loss in rel. efficiency when single economic weights are affected by error

% ERROR	VARAGG.	VARIND.	$\Delta\hat{H}$	$\Delta H\|\hat{I}$	LRE(%)
ERROR IN EC. WEIGHT OF : AV.D.GAIN					
-200	4.4107	0.9719	0.9858	0.9765	10.14
-150	4.4170	0.9815	0.9907	1.0268	5.51
-100	4.5011	1.0195	1.0097	1.0615	2.32
-50	4.6630	1.0860	1.0421	1.0808	0.54
0	4.9026	1.1809	1.0867	1.0867	0.00
50	5.2199	1.3042	1.1420	1.0818	0.45
100	5.6151	1.4559	1.2066	1.0691	1.62
150	6.0880	1.6360	1.2791	1.0512	3.27
200	6.6386	1.8446	1.3582	1.0301	5.21
ERROR IN EC. WEIGHT OF : FEED EFF.					
-200	2.5062	0.2185	0.4674	0.2561	76.44
-150	2.5534	0.2416	0.4915	0.7833	27.92
-100	2.9685	0.4097	0.6401	1.0160	6.51
-50	3.7516	0.7228	0.8502	1.0769	0.90
0	4.9026	1.1809	1.0867	1.0867	0.00
50	6.4215	1.7840	1.3357	1.0827	0.36
100	8.3084	2.5321	1.5913	1.0756	1.02
150	10.5632	3.4252	1.8507	1.0681	1.71
200	13.1859	4.4633	2.1126	1.0613	2.34
ERROR IN EC. WEIGHT OF : B.FAT(CARCASS)					
-200	4.2552	0.8800	0.9381	0.9933	8.59
-150	4.3418	0.9183	0.9583	1.0374	4.54
-100	4.4786	0.9812	0.9905	1.0665	1.86
-50	4.6655	1.0687	1.0338	1.0821	0.42
0	4.9026	1.1809	1.0867	1.0867	0.00
50	5.1897	1.3177	1.1479	1.0829	0.34
100	5.5270	1.4792	1.2162	1.0733	1.23
150	5.9144	1.6654	1.2905	1.0598	2.48
200	6.3520	1.8762	1.3697	1.0439	3.93

Table 14. Continued

% ERROR	VARAGG.	VARIND.	$\Delta\hat{H}$	$\Delta H\|\hat{I}$	LRE(%)
ERROR IN EC. WEIGHT OF : DRESSING %					
-200	4.3444	1.0799	1.0392	0.9760	10.19
-150	4.2563	1.0615	1.0303	1.0248	5.70
-100	4.3199	1.0723	1.0355	1.0599	2.47
-50	4.5353	1.1121	1.0545	1.0803	0.59
0	4.9026	1.1809	1.0867	1.0867	0.00
50	5.4216	1.2788	1.1308	1.0811	0.51
100	6.0925	1.4057	1.1856	1.0663	1.88
150	6.9151	1.5617	1.2497	1.0450	3.84
200	7.8896	1.7467	1.3216	1.0196	6.17
ERROR IN EC. WEIGHT OF : % LOIN + HAM					
-200	3.5300	0.6400	0.8000	0.9377	13.71
-150	3.6495	0.7151	0.8456	1.0144	6.65
-100	3.9181	0.8303	0.9112	1.0596	2.49
-50	4.3358	0.9856	0.9927	1.0810	0.52
0	4.9026	1.1809	1.0867	1.0867	0.00
50	5.6184	1.4163	1.1901	1.0828	0.36
100	6.4834	1.6918	1.3007	1.0735	1.22
150	7.4974	2.0074	1.4168	1.0615	2.32
200	8.6605	2.3630	1.5372	1.0484	3.52
ERROR IN EC. WEIGHT OF : LOIN EYE					
-200	4.0563	0.9565	0.9780	1.0503	3.35
-150	4.2029	0.9970	0.9985	1.0672	1.79
-100	4.3928	1.0480	1.0237	1.0785	0.75
-50	4.6260	1.1092	1.0532	1.0848	0.18
0	4.9026	1.1809	1.0867	1.0867	0.00
50	5.2225	1.2629	1.1238	1.0850	0.16
100	5.5858	1.3553	1.1642	1.0804	0.58
150	5.9924	1.4580	1.2075	1.0734	1.22
200	6.4423	1.5712	1.2535	1.0647	2.02

Table 14. Continued

% ERROR	VARAGG.	VARIND.	$\Delta\hat{H}$	$\Delta H\|\hat{I}$	LRE(%)
ERROR IN EC. WEIGHT OF : AV.#WEANED					
-200	4.9026	1.1809	1.0867	1.0110	6.96
-150	3.6693	1.1501	1.0724	1.0437	3.96
-100	3.2583	1.1398	1.0676	1.0676	1.76
-50	3.6693	1.1501	1.0724	1.0820	0.43
0	4.9026	1.1809	1.0867	1.0867	0.00
50	6.9579	1.2323	1.1101	1.0823	0.40
100	9.8355	1.3042	1.1420	1.0700	1.53
150	13.5352	1.3967	1.1818	1.0514	3.25
200	18.0570	1.5097	1.2287	1.0280	5.40

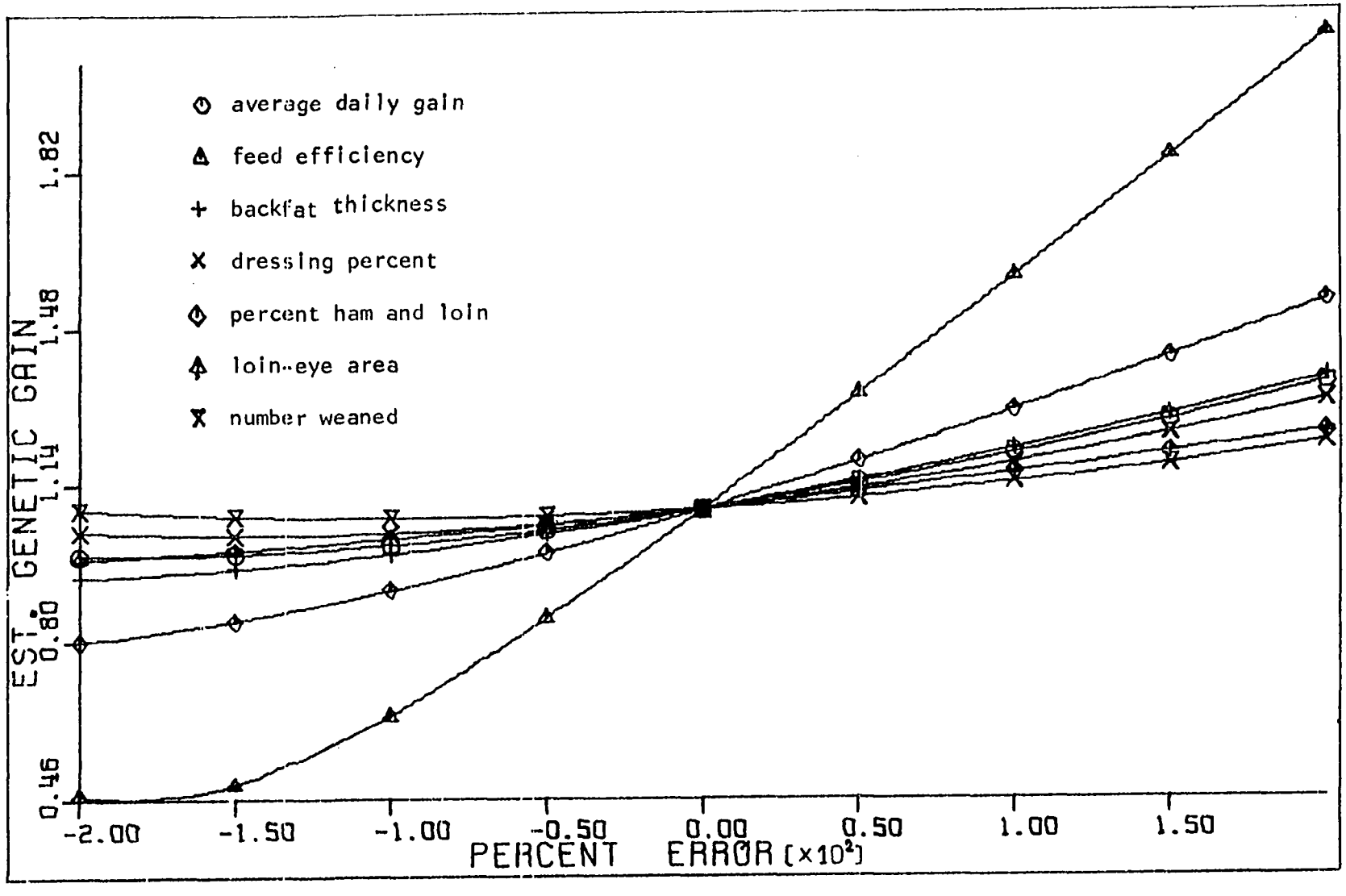


Figure 1. Estimated genetic gain ($\Delta\hat{H}$) when single economic weights are affected by errors ranging from minus 200 percent to plus 200 percent

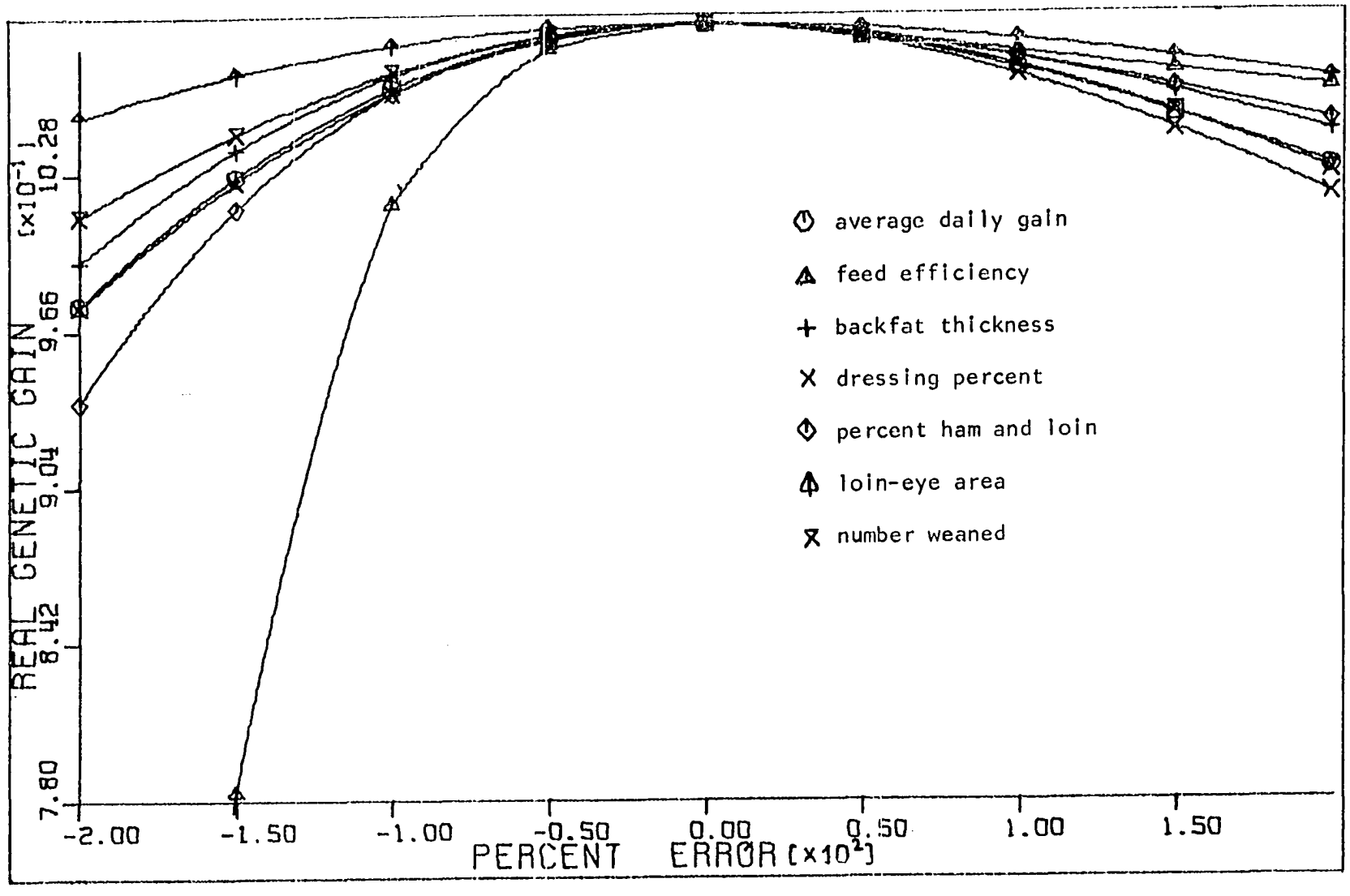


Figure 2. Real genetic gain ($\Delta H|\hat{I}$) when single economic weights are affected by errors ranging from minus 200 percent to plus 200 percent

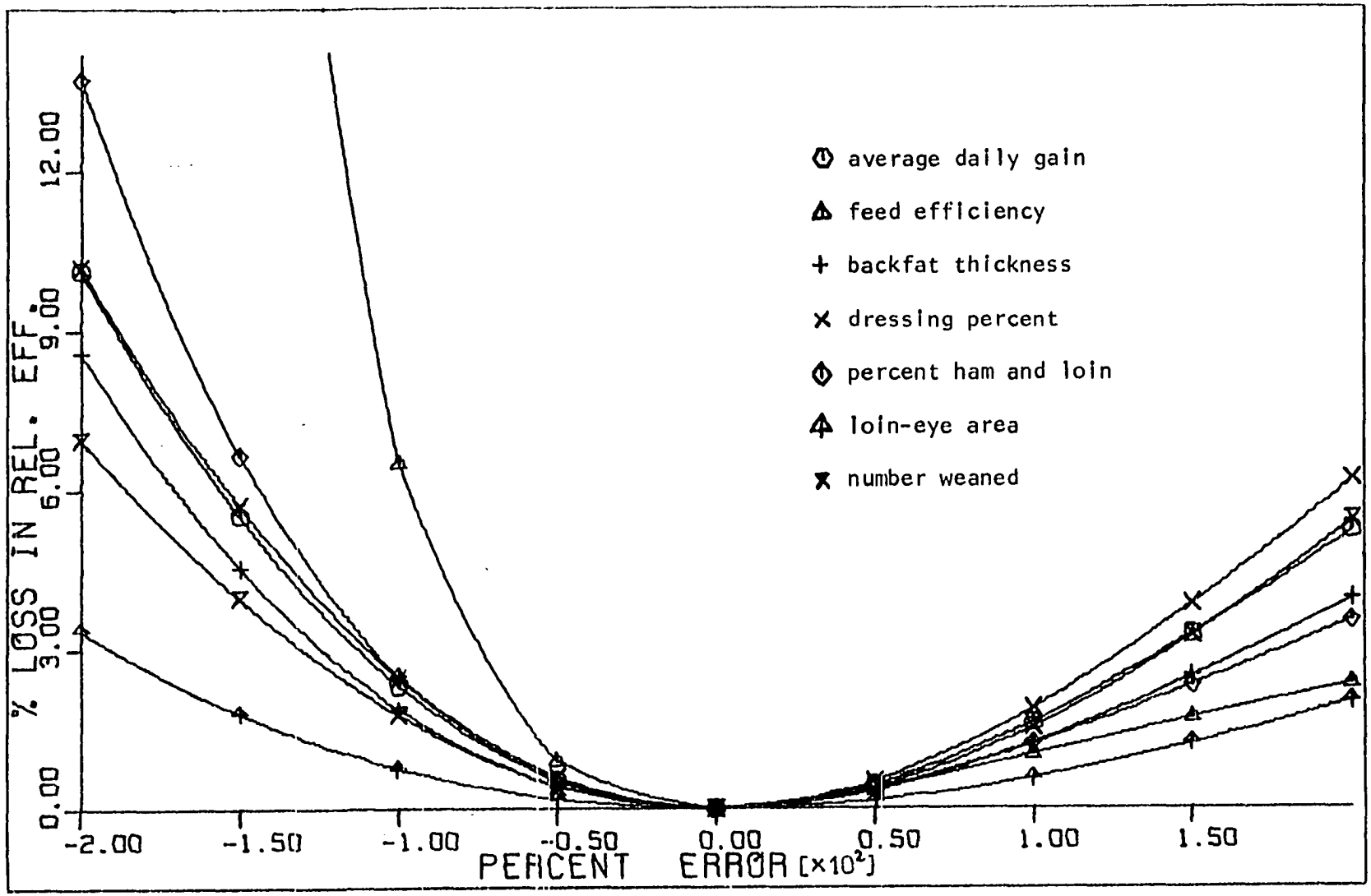


Figure 3. Loss in relative efficiency (LRE) when single economic weights are affected by errors ranging from minus 200 percent to plus 200 percent

Table 15. Correlation of each trait in agg. genotype with index when single economic weights are affected by error

% ERROR	-200	-150	-100	-50	0	50	100	150	200
TRAIT									
ERROR IN EC. WEIGHT OF : AV.D.GAIN									
1	-0.0118	0.0610	0.1312	0.1963	0.2546	0.3053	0.3487	0.3853	0.4159
2	-0.4184	-0.4683	-0.5105	-0.5441	-0.5692	-0.5867	-0.5980	-0.6044	-0.6071
3	-0.4707	-0.4505	-0.4245	-0.3943	-0.3619	-0.3289	-0.2966	-0.2660	-0.2375
4	0.1638	0.1604	0.1549	0.1476	0.1392	0.1302	0.1212	0.1123	0.1039
5	0.4542	0.4385	0.4171	0.3913	0.3630	0.3337	0.3048	0.2771	0.2511
6	0.3168	0.3023	0.2839	0.2627	0.2401	0.2173	0.1950	0.1739	0.1543
7	0.0325	0.0324	0.0317	0.0308	0.0295	0.0281	0.0266	0.0251	0.0236
ERROR IN EC. WEIGHT OF : FEED EFF.									
1	-0.3671	-0.1212	0.0820	0.1936	0.2546	0.2910	0.3147	0.3311	0.3431
2	0.1232	-0.2268	-0.4382	-0.5287	-0.5692	-0.5896	-0.6012	-0.6082	-0.6128
3	-0.1809	-0.3290	-0.3732	-0.3718	-0.3619	-0.3522	-0.3442	-0.3376	-0.3323
4	0.1654	0.1949	0.1786	0.1562	0.1392	0.1271	0.1183	0.1117	0.1066
5	0.3157	0.4258	0.4234	0.3913	0.3630	0.3415	0.3254	0.3132	0.3036
6	0.3321	0.3696	0.3251	0.2759	0.2401	0.2152	0.1972	0.1839	0.1736
7	0.0686	0.0652	0.0501	0.0377	0.0295	0.0240	0.0201	0.0173	0.0152

Table 15. Continued

% ERROR	-200	-150	-100	-50	0	50	100	150	200
TRAIT									
ERROR IN EC. WEIGHT OF : B.FAT(CARCASS)									
1	0.3554	0.3331	0.3079	0.2813	0.2546	0.2286	0.2041	0.1814	0.1605
2	-0.5379	-0.5563	-0.5669	-0.5708	-0.5692	-0.5637	-0.5554	-0.5455	-0.5348
3	-0.0872	-0.1666	-0.2398	-0.3051	-0.3619	-0.4104	-0.4514	-0.4858	-0.5145
4	0.2159	0.1980	0.1786	0.1587	0.1392	0.1206	0.1033	0.0874	0.0730
5	0.2786	0.3075	0.3310	0.3494	0.3630	0.3726	0.3790	0.3830	0.3851
6	0.1672	0.1908	0.2109	0.2273	0.2401	0.2500	0.2574	0.2627	0.2665
7	0.0342	0.0335	0.0324	0.0310	0.0295	0.0279	0.0264	0.0248	0.0234
ERROR IN EC. WEIGHT OF : DRESSING %									
1	0.2799	0.2788	0.2740	0.2657	0.2546	0.2415	0.2273	0.2128	0.1986
2	-0.5495	-0.5658	-0.5744	-0.5753	-0.5692	-0.5575	-0.5417	-0.5235	-0.5040
3	-0.4643	-0.4466	-0.4229	-0.3941	-0.3619	-0.3280	-0.2941	-0.2611	-0.2301
4	-0.0573	-0.0067	0.0443	0.0935	0.1392	0.1804	0.2165	0.2476	0.2740
5	0.3177	0.3360	0.3499	0.3588	0.3630	0.3630	0.3598	0.3542	0.3471
6	0.2233	0.2322	0.2381	0.2406	0.2401	0.2372	0.2323	0.2262	0.2193
7	0.0308	0.0311	0.0310	0.0304	0.0295	0.0283	0.0270	0.0257	0.0243

Table 15. Continued

% ERROR	-200	-150	-100	-50	0	50	100	150	200
TRAIT									
ERROR IN EC. WEIGHT OF : % LOIN + HAM									
1	0.4381	0.3926	0.3441	0.2973	0.2546	0.2169	0.1843	0.1561	0.1319
2	-0.5767	-0.5921	-0.5926	-0.5835	-0.5692	-0.5528	-0.5360	-0.5198	-0.5046
3	-0.2047	-0.2615	-0.3057	-0.3384	-0.3619	-0.3787	-0.3906	-0.3990	-0.4051
4	0.1095	0.1224	0.1311	0.1363	0.1392	0.1405	0.1408	0.1405	0.1399
5	0.1260	0.2060	0.2718	0.3234	0.3630	0.3931	0.4161	0.4338	0.4476
6	0.0842	0.1369	0.1802	0.2141	0.2401	0.2600	0.2751	0.2867	0.2957
7	0.0401	0.0379	0.0352	0.0323	0.0295	0.0269	0.0246	0.0226	0.0209
ERROR IN EC. WEIGHT OF : LOIN EYE									
1	0.3220	0.3058	0.2889	0.2718	0.2546	0.2376	0.2212	0.2053	0.1901
2	-0.5953	-0.5922	-0.5865	-0.5787	-0.5692	-0.5585	-0.5469	-0.5348	-0.5224
3	-0.3031	-0.3211	-0.3369	-0.3504	-0.3619	-0.3715	-0.3794	-0.3858	-0.3910
4	0.1389	0.1399	0.1402	0.1400	0.1392	0.1381	0.1366	0.1349	0.1330
5	0.2966	0.3166	0.3343	0.3497	0.3630	0.3742	0.3836	0.3915	0.3980
6	0.1228	0.1559	0.1861	0.2143	0.2401	0.2636	0.2847	0.3036	0.3206
7	0.0328	0.0321	0.0313	0.0304	0.0295	0.0285	0.0275	0.0265	0.0256

Table 15. Continued

% ERROR	-200	-150	-100	-50	0	50	100	150	200
TRAIT									
ERROR IN EC. WEIGHT OF : AV.#WEANED									
1	0.2546	0.2580	0.2591	0.2580	0.2546	0.2492	0.2422	0.2341	0.2251
2	-0.5692	-0.5768	-0.5794	-0.5768	-0.5692	-0.5572	-0.5416	-0.5234	-0.5034
3	-0.3619	-0.3667	-0.3684	-0.3667	-0.3619	-0.3543	-0.3444	-0.3328	-0.3201
4	0.1392	0.1411	0.1417	0.1411	0.1392	0.1363	0.1325	0.1280	0.1231
5	0.3630	0.3678	0.3695	0.3678	0.3630	0.3553	0.3454	0.3337	0.3210
6	0.2401	0.2433	0.2444	0.2433	0.2401	0.2351	0.2285	0.2208	0.2124
7	-0.0295	-0.0149	0.0	0.0149	0.0295	0.0433	0.0561	0.0678	0.0783

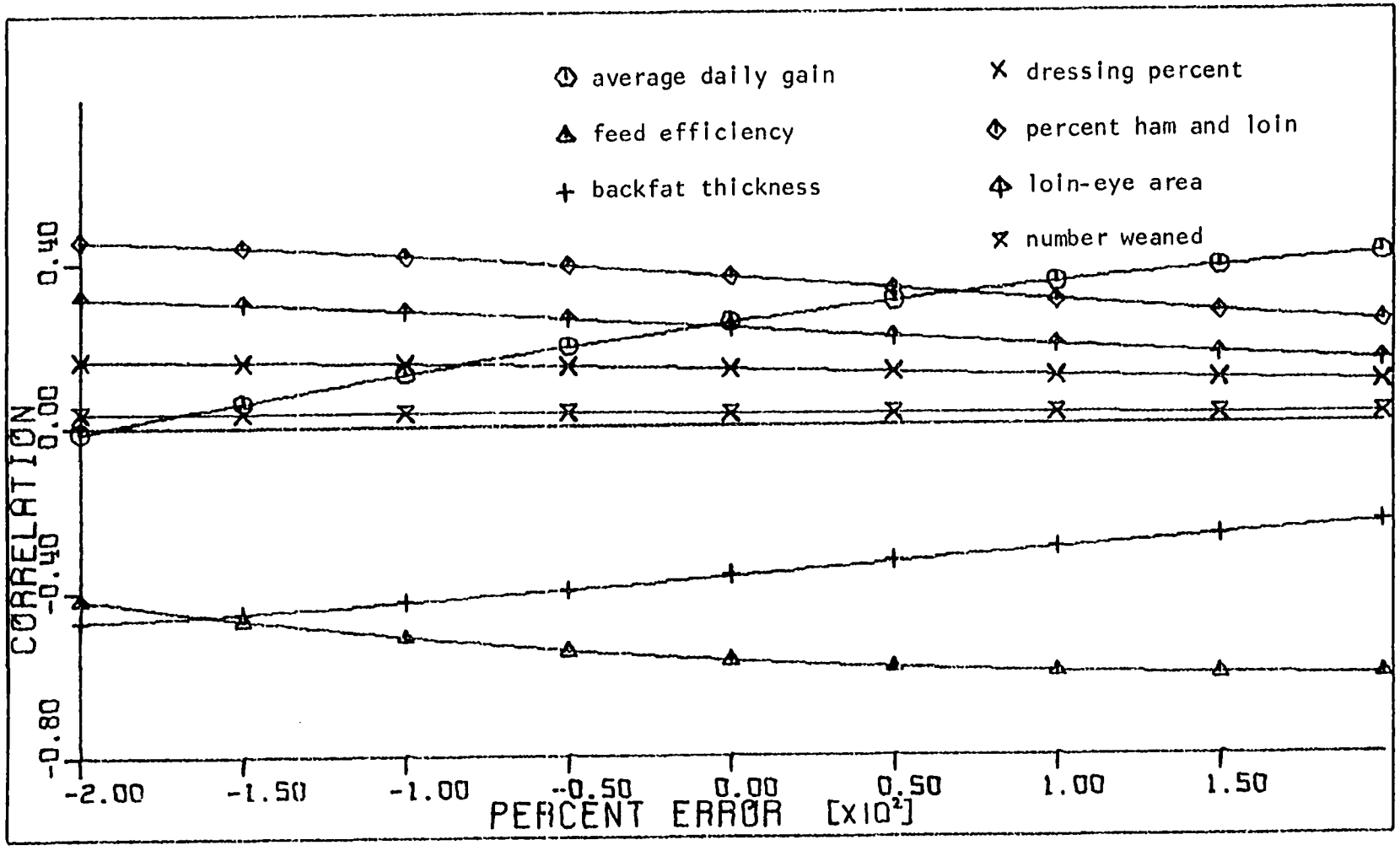


Figure 4. Correlations of index with breeding values as affected by errors in economic weight of average daily gain

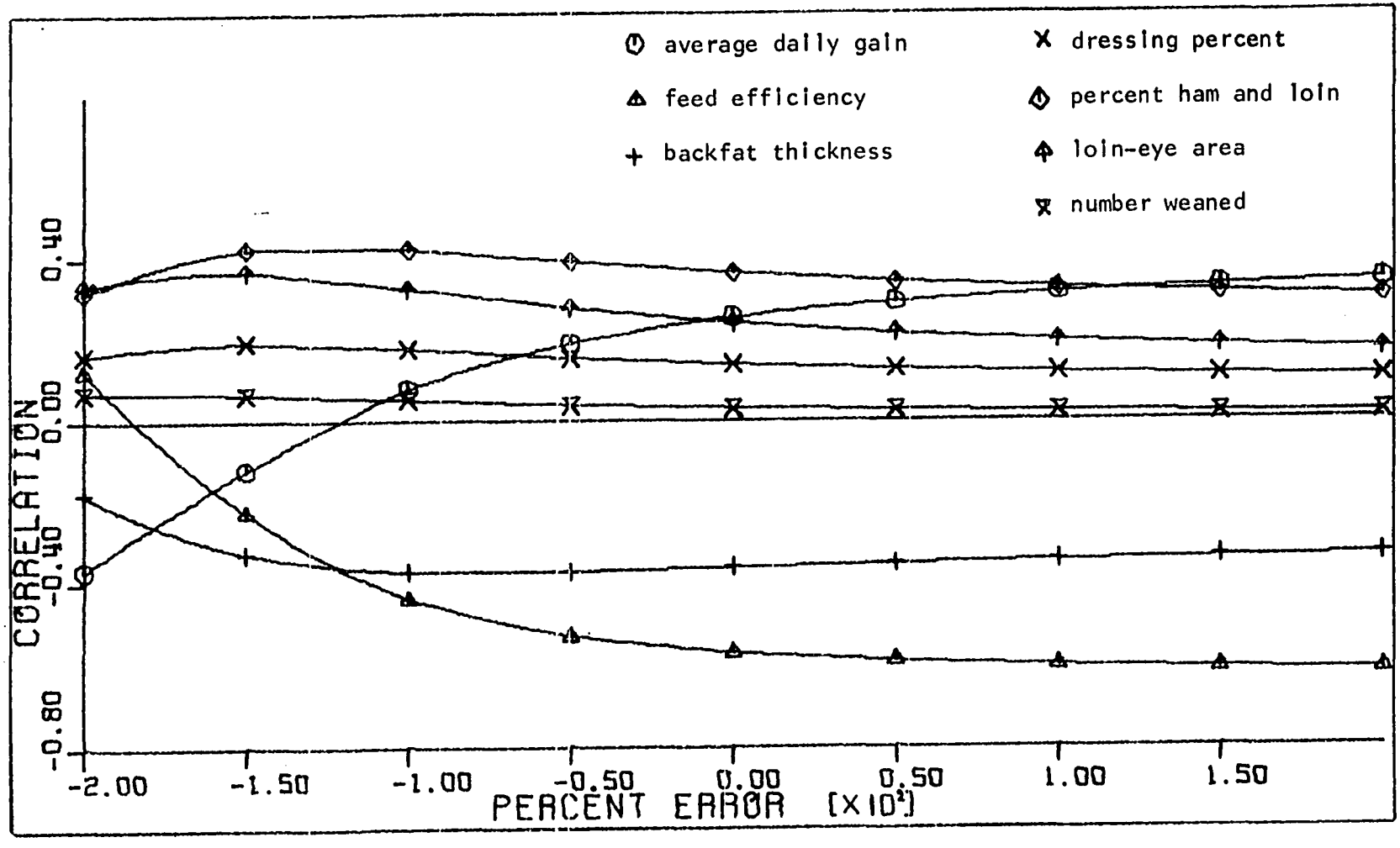


Figure 5. Correlations of index with breeding values as affected by errors in economic weight of feed efficiency

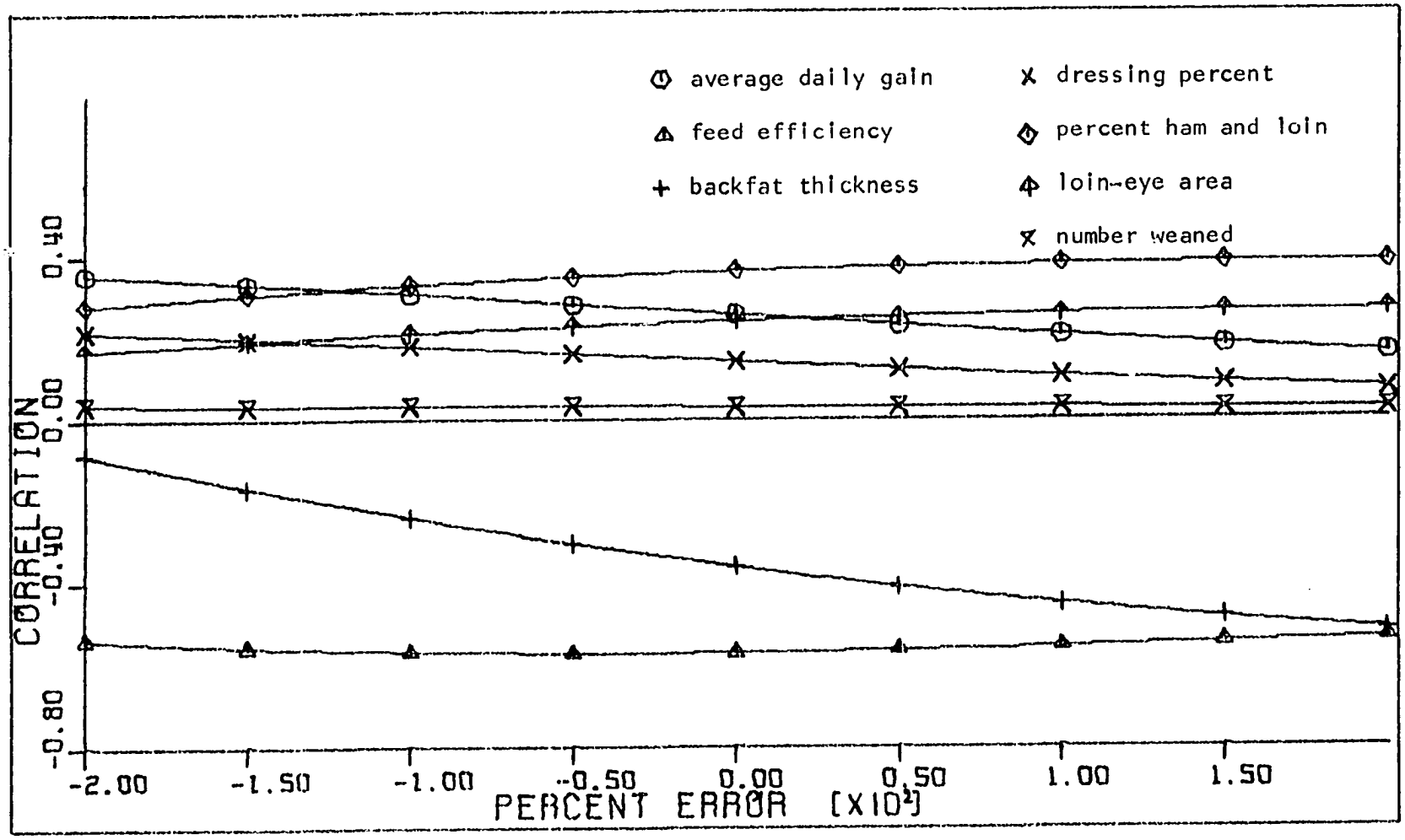


Figure 6. Correlations of index with breeding values as affected by errors in economic weight of backfat thickness

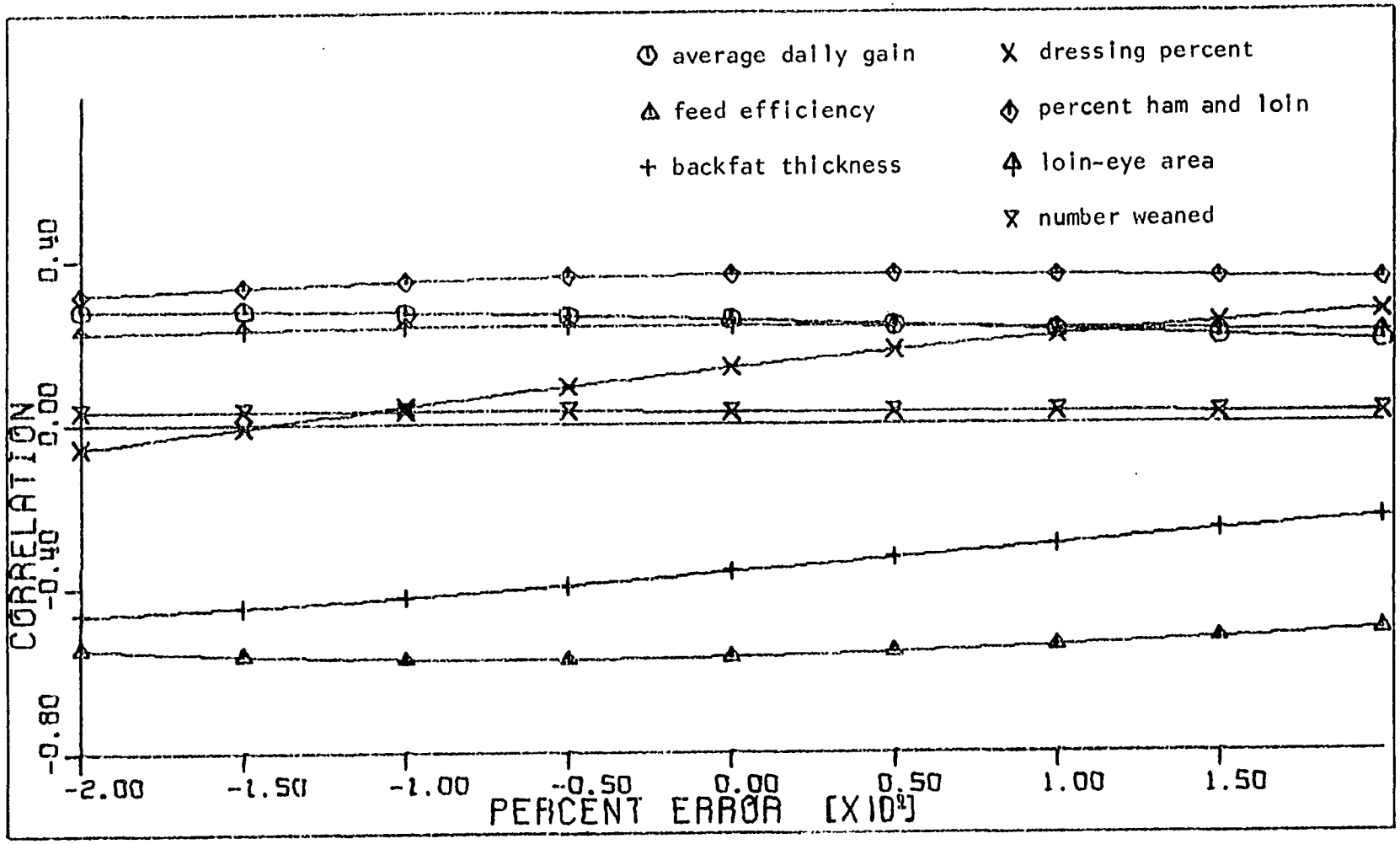


Figure 7. Correlations of index with breeding values as affected by errors in economic weight of dressing percent

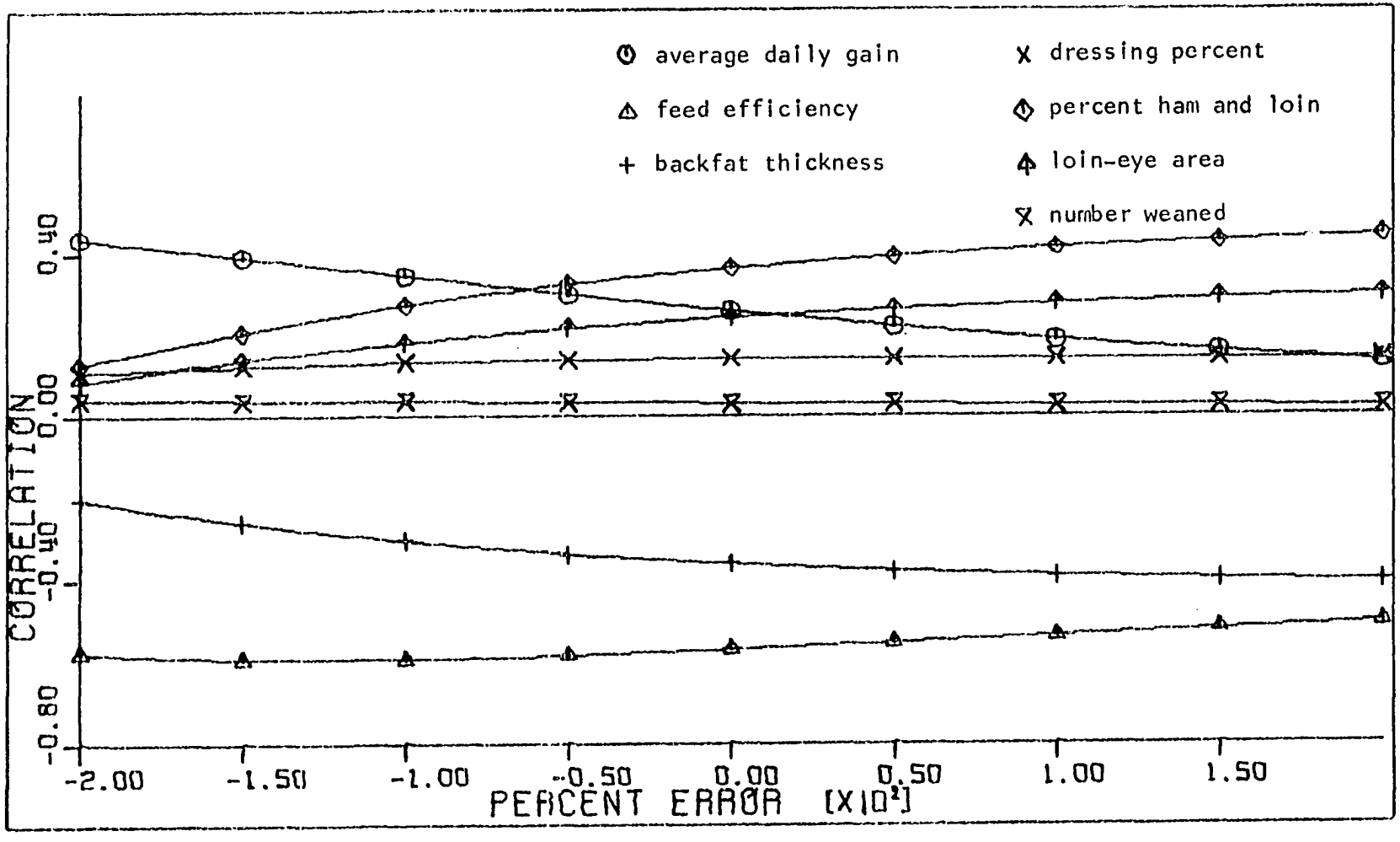


Figure 8. Correlations of index with breeding values as affected by errors in economic weight of percent ham and loin

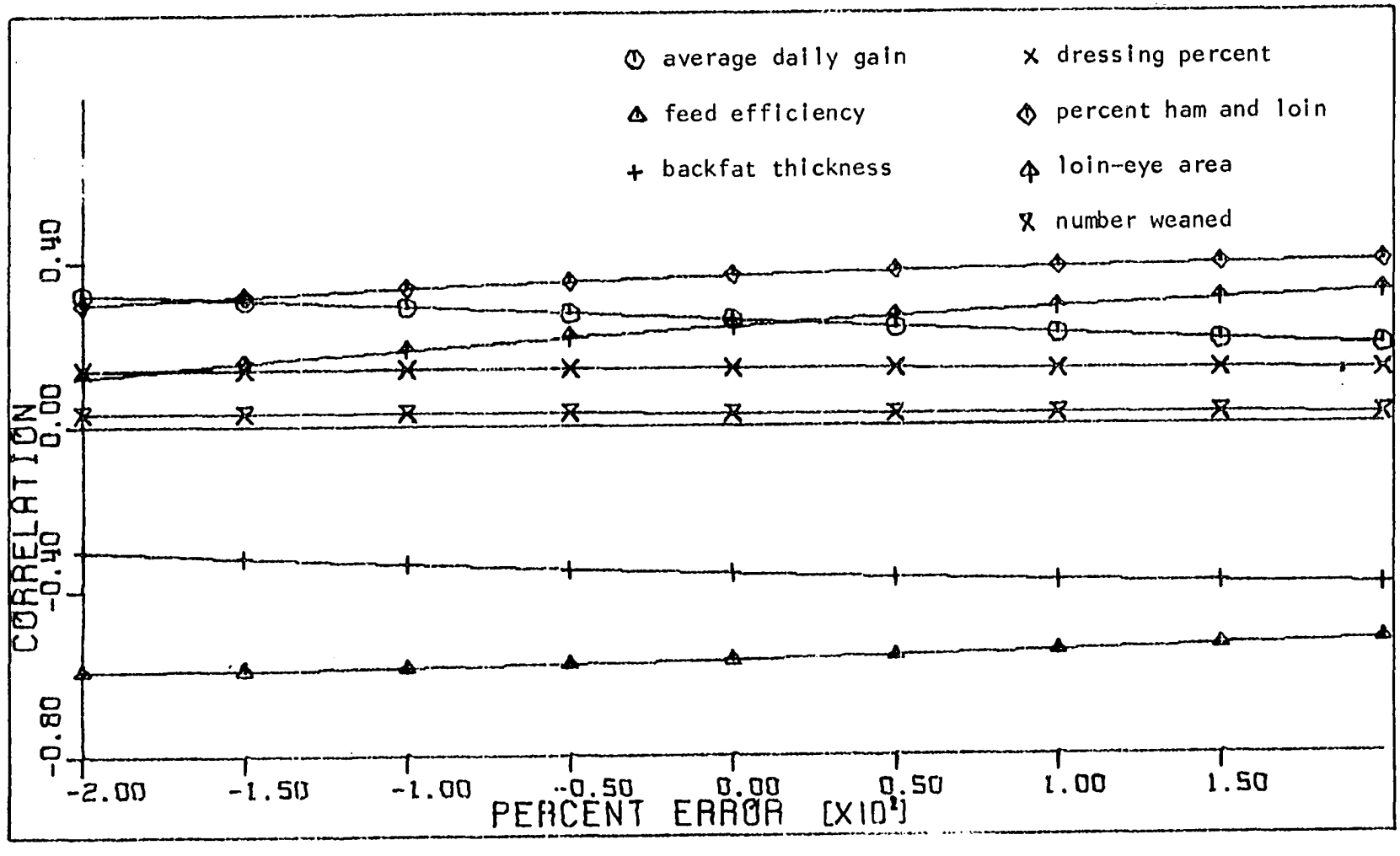


Figure 9. Correlations of index with breeding values as affected by errors in economic weight of loin-eye area

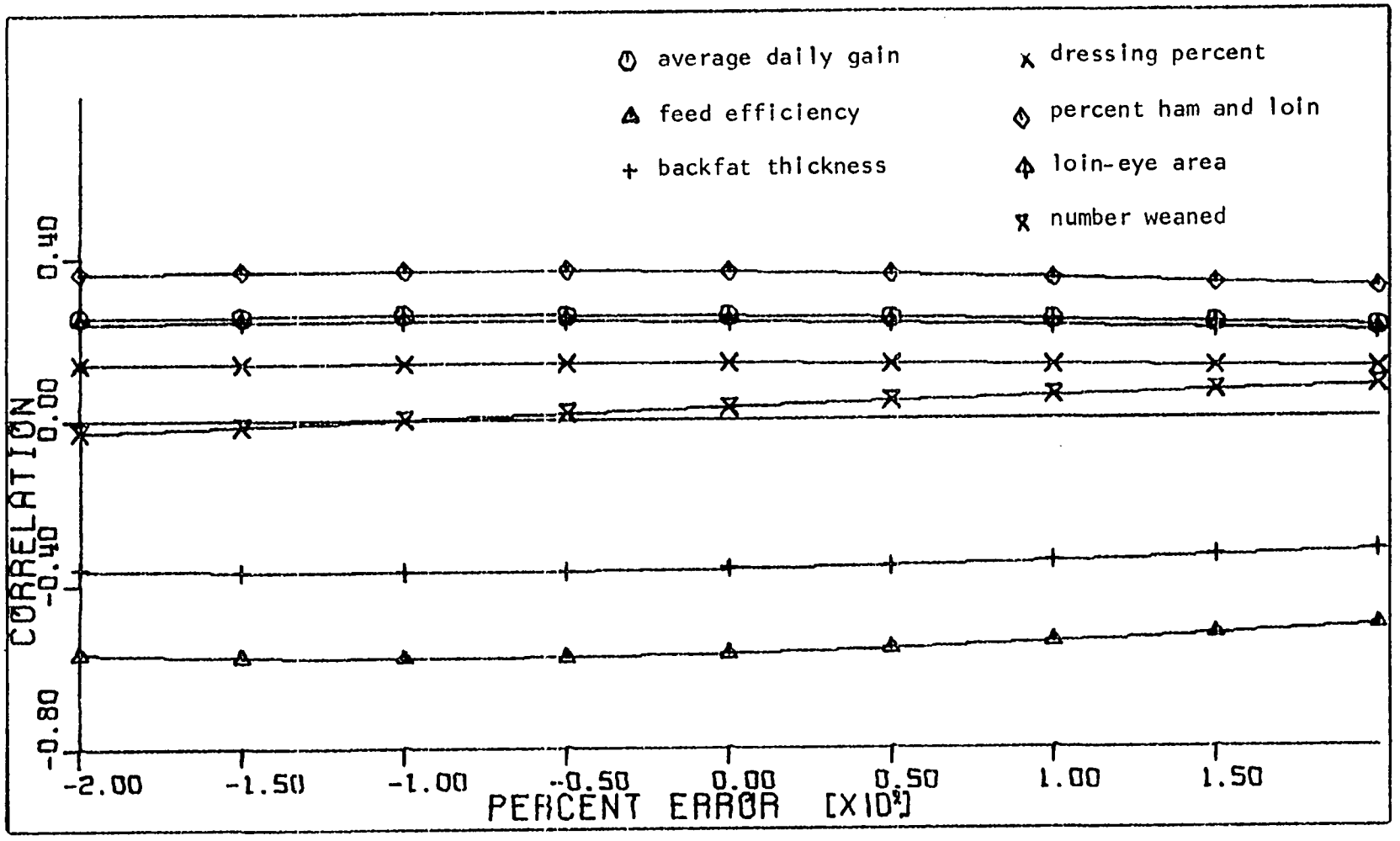


Figure 10. Correlations of index with breeding values as affected by errors in economic weight of number weaned

trait j, $R(IG_j)$ can be made zero or changed of sign. This could be used to restrict selection indexes.

4. Random errors in the economic weight vector

The effects of errors in single economic weights were considered in Section 2. This approach was used to study the effects of errors in economic weights that are difficult to estimate accurately (i.e., loin-eye area). In reality, however, all economic weights are subject to error simultaneously and will simultaneously affect real and estimated genetic gain.

a. Simulation of random errors and index samples In cases where complete information is available, economic weights can be estimated by multiple regression technique and the variances and covariances of the regression coefficients (economic weights) can be calculated. Since this vital information could not be produced, Monte-Carlo simulation was used to study the effect of random errors in the economic weight vector on real and estimated genetic gain and the loss in relative efficiency.

Errors were introduced in the economic weight vector in the following way: $\hat{a} = a(1 + \varepsilon)$, where a is the vector of economic weights used previously and ε is a vector of random errors that are $NID(0,\sigma^2_\varepsilon)$. It is easily demonstrated that the new economic weights, $a(1 + \varepsilon)$, are unbiased and have variance $a^2\sigma^2_\varepsilon$.

Four random samples (with sample size N = 100) of economic weight vectors were generated. The random errors were drawn from normal distributions with standard deviations (σ_ε) of 0.1, 0.2, 0.5 and 1.0, respectively. Each sample of economic weight vectors resulted in 100 selection

indexes. The major distribution statistics of each sample were calculated for $\Delta\hat{H}$, $\Delta H|\hat{I}$, LRE, and are listed in Table 16.

b. Derivations of expectations and variances To relate the errors in the estimated economic weights to the variances and expectations of $\Delta\hat{H}$, $\Delta H|\hat{I}$ and LRE and to get a better insight in the mathematics involved, an attempt was made to derive expectations and variances for the generated distributions.

Expectations and variances of complex functions of the general form $(x'Ax)^{1/2}$, $\frac{x'Ay}{(x'Ax)^{1/2}}$ (where x and y are vectors of random variables and A is a matrix of constants) can only be derived by approximation. Kendall and Stuart (1958) suggested the use of the first terms of a Taylor's expansion.

Let $g(x_1,x_2,\ldots,x_k)$ be a function of variables x_1, x_2, ..., x_k and assume that x_i have means m_i, finite variances and be differentiable at $x_i = m_i$. Then the expansion of g is:

$$g(x_1,x_2,\ldots,x_k) = g(m_1,m_2,\ldots,m_k)$$

$$+ \sum_{i=1}^{k} \frac{\partial g}{\partial m_i} \Delta x_i + \frac{1}{2} \sum_{i,j=1}^{k} \frac{\partial^2 g}{\partial m_i \partial m_j} \Delta x_i \Delta x_j + O(\Delta x)^3$$

where:

(a) $\frac{\partial g}{\partial m_i}$ indicates the first partial derivative of g with respect to x_i, evaluated at $x_i=m_i$ for all values of i.

Table 16. Major distribution statistics of $\Delta\hat{H}$, $\Delta H|\hat{I}$ and LRE for four generated index samples (N = 100)

Sampling error(σ_ε)	Exp. val.[a]	Variance[a]	Std. dev.	Min. val.	Max. val.	β_1[b]	β_2[c]
Estimated genetic gain ($\Delta\hat{H}$)							
0.10	1.09085	0.00371	0.06093	0.97509	1.30509	0.21468	3.52099
	1.08800	0.00312					
0.20	1.09779	0.01483	0.12178	0.86549	1.52519	0.21245	3.51258
	1.09197	0.01237					
0.50	1.13562	0.09016	0.30027	0.56059	2.19149	0.22192	3.54848
	1.12168	0.07280					
1.00	1.26717	0.30964	0.55645	0.25929	3.30909	0.40114	3.87259
	1.24036	0.24727					
Real genetic gain ($\Delta H|\hat{I}$)							
0.10	1.08529	0.00000	0.00132	1.07999	1.08669	4.07848	8.17399
	1.08538	0.00000					
0.20	1.08115	0.00002	0.00453	1.06199	1.08669	3.91379	7.74180
	1.08135	0.00009					
0.50	1.05008	0.00110	0.03323	0.88799	1.08659	4.82347	9.19628
	1.04990	0.00343					
1.00	0.90005	0.05137	0.22665	-0.10189	1.08449	4.73826	7.72679
	0.92472	0.04269					

[a]The upper value of each pair is the simulated estimate, while the lower value is derived from the approximate equation.

[b]β_1 measures skewness, for the normal distribution $\beta_1 = 0$.

[c]β_2 measures kurtosis, for the normal distribution $\beta_2 = 3$.

Table 16. Continued

Sampling error (σ_ε)	Exp. val.[a]	Variance[a]	Std. dev.	Min. val.	Max. val.	β_1[b]	β_2[c]
Loss in relative efficiency (LRE)							
0.10	0.12738	0.01087	0.10427	0.00059	0.61979	4.19367	8.32184
	0.12059	0.04972					
0.20	0.50805	0.17409	0.41724	0.00089	2.27009	3.92706	7.75134
	0.49146	0.78966					
0.50	2.61190	10.82238	3.28974	0.00105	18.28739	4.21573	8.54555
	3.37830	29.09834					
1.00	17.17443	435.05249	20.85791	0.20559	109.37959	4.73878	7.72721
	14.90486	361.55920					

(b) $\Delta x_i = x_i - m_i$ and $E(\Delta x_i) = 0$ for all i

$$E(\Delta x_i \Delta x_j) = Cov(x_i x_j) \text{ for } i \neq j$$

(c) $O(\Delta x)^3$ indicates the remaining terms of order $(\Delta x)^3$ and higher.

The expected value of g is:

$$E(g) \doteq g(m_1, m_2, \ldots, m_k) + \frac{1}{2} \sum_{i,j=1}^{k} \frac{\partial^2 g}{\partial m_i \partial m_j} Cov(x_i, x_j) \tag{65}$$

The symbol $\doteq$ means "is approximately equal to", and

$$\frac{\partial^2 g}{\partial m_i \partial m_j}$$

indicates the second partial derivative of g, first with respect to x_i then with respect to x_j evaluated at $x_i = m_i$ for all i. This is an approximation because of omitting terms of third and higher order.

$$V(g) \doteq \sum_{i,j=1}^{k} \frac{\partial g}{\partial m_i} \frac{\partial g}{\partial m_j} Cov(x_i, x_j) \; . \tag{66}$$

In a similar manner it can be shown that the covariance between two functions of random variables, say g and h is:

$$Cov(g,h) \doteq \sum_{i,j=1}^{k} \frac{\partial g}{\partial m_i} \frac{\partial h}{\partial m_j} Cov(x_i, x_j) \; . \tag{67}$$

The accuracy of these approximations depends on the smallness of the higher order terms of the expansion which are dropped. This method is only useful in cases where the Taylor series is converging at a relatively fast rate.

Application of these formulas leads to the following general results:

$$E\left(\frac{x}{y}\right) \doteq \frac{E(x)}{E(y)}\left[1 + \frac{V(y)}{E^2(y)} - \frac{Cov(x,y)}{E(x)E(y)}\right]$$

$$V\left(\frac{x}{y}\right) \doteq \frac{E^2(x)}{E^2(y)}\left[\frac{V(x)}{E^2(x)} + \frac{V(y)}{E^2(y)} - 2\frac{Cov(x,y)}{E(x)E(y)}\right]$$

$$Cov\left(x,\frac{y}{z}\right) \doteq \frac{Cov(x,y)}{E(z)} - \frac{E(y)Cov(x,z)}{E^2(z)}$$

$$E(xy) = E(x)E(y) + Cov(x,y)$$

$$V(xy) \doteq E^2(y)V(x) + E^2(x)V(y) + 2E(x)E(y)Cov(x,y)$$

$$E(x^{1/2}) \doteq E^{1/2}(x)\left[1 - \frac{V(x)}{8E^2(x)}\right]$$

$$V(x^{1/2}) \doteq \frac{V(x)}{4E(x)}$$

$$Cov(x,y^{1/2}) \doteq \frac{Cov(x,y)}{2E^{1/2}(y)} \qquad \text{and}$$

$$Cov(x^{1/2},y^{1/2}) \doteq \frac{Cov(x,y)}{4E^{1/2}(x)E^{1/2}(y)} \; .$$

We want to derive approximations for the expected values and variances of $\Delta\hat{H}$, $\Delta H|\hat{I}$ and LRE, and will further assume that the selection differential equals σI; the genetic parameters and the economic weights in the correct

aggregate genotype are known constants, and that the economic weights have the same error structure ($\hat{a} = a(1+\varepsilon)$) as the one used for the simulation.

(a) $\Delta\hat{H} = V^{1/2}(\hat{I})$

$$E[V^{1/2}(\hat{I})] \doteq E^{1/2}[V(\hat{I})]\ [1 - \frac{V[V(\hat{I})]}{8E^2[V(\hat{I})]}] \tag{68a}$$

$$V[V^{1/2}(\hat{I})] \doteq \frac{V[V(\hat{I})]}{4E[V(\hat{I})]} \tag{68b}$$

(b) $\Delta H|\hat{I} = \frac{Cov_c(\hat{I},H)}{V_c^{1/2}(\hat{I})}$

$$E[\Delta H|\hat{I}] \doteq \frac{E[Cov_c(\hat{I},H)]}{E[V_c^{1/2}(\hat{I})]}\ [\ 1 + \frac{V[V_c^{1/2}(\hat{I})]}{E^2[V_c^{1/2}(\hat{I})]} - \frac{Cov[Cov_c(\hat{I},H),V_c^{1/2}(\hat{I})]}{E[Cov_c(\hat{I},H)]\ E[V_c^{1/2}(\hat{I})]}\ ]$$

$$\doteq \frac{E[Cov_c(\hat{I},H)]}{E^{1/2}[V_c(\hat{I})][1 - \frac{V[V_c(\hat{I})]}{8E^2[V_c(\hat{I})]}]}\ \{1 + \frac{V[V_c(\hat{I})]}{4E^2[V_c(\hat{I})]\{1 - \frac{V[V_c(\hat{I})]}{8E^2[V_c(\hat{I})]}\}^2}$$

$$- \frac{Cov[Cov_c(\hat{I},H),V_c(\hat{I})]}{2E[Cov(\hat{I},H)]E[V_c(\hat{I})]\ [1 - \frac{V[V_c(\hat{I})]}{8E^2[V_c(\hat{I})]}]}\ \} \tag{69a}$$

$V_c(\ )$, and $Cov_c(\ )$ are the conditional variances and covariances

(given $I = \hat{I}$), while E[ ], V[ ] and Cov[ ] indicate the expectation, variance and covariance respectively of the values in the brackets over the population of calculated indexes from repeated sampling of the economic weights.

$$V[\Delta H|\hat{I}] = V\left[\frac{Cov_c(\hat{I},H)}{V_c^{1/2}(\hat{I})}\right]$$

$$\doteq \left\{\frac{E^2[Cov_c(\hat{I},H)]}{E^2[V_c^{1/2}(\hat{I})]}\right. \left[\frac{V[Cov_c(\hat{I},H)}{E^2[Cov_c(\hat{I},H)} + \frac{V[V_c^{1/2}(\hat{I})]}{E^2[V_c^{1/2}(\hat{I})]}\right.$$

$$\left. - 2\,\frac{Cov[Cov_c(\hat{I},H), V_c^{1/2}(\hat{I})]}{E[Cov_c(\hat{I},H)]E[V_c^{1/2}(\hat{I})]}\right]$$

$$\doteq \frac{E^2[Cov_c(\hat{I},H)]}{E[V_c(\hat{I})]\left[1 - \frac{V[V_c(\hat{I})]}{8E^2[V_c(\hat{I})]}\right]^2} \left\{\frac{V[Cov_c(\hat{I},H)]}{E^2[Cov_c(\hat{I},H)]}\right.$$

$$+ \frac{V[V_c(\hat{I})]}{4E^2[V_c(\hat{I})]\left[1 - \frac{V[V_c(\hat{I})]}{8E^2[V_c(\hat{I})]}\right]^2}$$

$$\left. - \frac{Cov[Cov_c(\hat{I},H),\ V_c(\hat{I})]}{E[Cov_c(\hat{I},H)]\ E[V_c(\hat{I})]\left[1 - \frac{V[V_c(\hat{I})]}{8E^2[V_c(\hat{I})]}\right]}\right\} \qquad (69b)$$

$$(c)\quad LRE = 100\left[\,1 - \frac{Cov_c(\hat{I},H)}{[V(I)\ V_c(\hat{I})]^{1/2}}\,\right]$$

$$E(LRE) = 100\left\{1 - \frac{1}{[V(I)]^{1/2}}\ E\left[\frac{Cov_c(\hat{I},H)}{V_c(\hat{I})^{1/2}}\right]\right\} \qquad (70a)$$

$E\left[\frac{Cov_c(\hat{I},H)}{V_c(\hat{I})^{1/2}}\right]$ has been derived under (b).

$$V(LRE) \doteq \frac{100^2}{V(I)}\ V\left[\frac{Cov_c(I,H)}{[V_c(I)]^{1/2}}\right] \qquad (70b)$$

$V\left[\frac{Cov_c(\hat{I},H)}{V_c(\hat{I})^{1/2}}\right]$ has been derived under (b).

To apply these formulas to our particular case we have first to develop them in terms of the assumed error structure of the economic weights. And in order to eliminate elaborate and tedious summations with confusing subscripts and superscripts, some theorems of matrix algebra will be applied to derive expectations, variances and covariances of matrixes of random variables (Searle, 1956 and 1971).

The symbol tr stands for trace, tr(A) is the sum of the diagonal elements of matrix A. Since a quadratic form is a scalar, it equals its own trace: $x'Ax = tr(x'Ax) = tr(Axx')$ where x is a vector of random variables and A is a matrix of constants.

Theorem: When $x = N(\mu,V)$ and A is a matrix of constants

$$E(x'Ax) = tr(AV) + \mu'A\mu$$

$$V(x'Ax) = 2tr(AV)^2 + 4\ \mu'AVA\ \mu$$

Corollary 1: When $x = N(\mu,V)$ and P and Q are matrices of constants

$$Cov(x'Px, x'Qx) = 2tr(PVQV) + 4\ \mu'PVQ\ \mu$$

Corollary 2: When $x_1 = N(\mu_1,V)$ and $x_2 = N(\mu_2,U)$

$$Cov(x_1'Px_1, x_2'Qx_2) = 2tr(PVQU) + 2\mu_1'PVQ\mu_1 + 2\mu_2'PUQ\mu_2$$

$$E[V(\hat{I})] = E[\hat{b}'P\hat{b}] = E[\hat{a}'G'P^{-1}\hat{a}]$$

let $G'P^{-1}G = A$ and $V(\hat{a}\hat{a}') = E(a\varepsilon\varepsilon'a') = \sigma_\varepsilon^2 U$

where U is a mxm matrix with the squared economic weights (a_i^2) in the diagonal and all off-diagonal elements zero.

$$= \sigma_\varepsilon^2\ tr(AU) + a'Aa$$

$$= \sigma_\varepsilon^2\ tr(AU) + V(I)$$

$$V[V(\hat{I})] = 2\ \sigma_\varepsilon^4 tr(AU)^2 + 4\ \sigma_\varepsilon^2(a'AUAa)$$

$$E[Cov_c(\hat{I},H)] = a'Aa = V(I)$$

$$V[Cov_c(\hat{I},H)] = \sigma_\varepsilon^2(a'AUAa)$$

$$Cov[Cov_c(\hat{I},H), V_c(\hat{I})] = 2\ \sigma_\varepsilon^2(a'AUAa)$$

These are the expectations, variances and covariances in terms of the

error structure of the economic weights that have to be substituted in formulas 68a, 68b, 69a, 69b, 70a and 70b. After the substitution we obtain:

$$\text{(a)}\quad E[V^{1/2}(\hat{I})] \doteq [V(I) + \sigma_\varepsilon^2\, tr(AU)]^{1/2}\ [1 - \frac{2\sigma_\varepsilon^2 tr(AU)^2 + 4\sigma_\varepsilon^2 (a'AUAa)}{8[V(I) + \sigma_\varepsilon^2\, tr(AU)]^2}] \quad (71a)$$

$$V[V^{1/2}(\hat{I})] \doteq \frac{\sigma_\varepsilon^4 tr(AU)^2 + 2\sigma_\varepsilon^2 (a'AUAa)}{2[V(I) + \sigma_\varepsilon^2\, tr(AU)]} \quad (71b)$$

$$\text{(b)}\quad E[\Delta H|\hat{I}] \doteq \frac{V(I)}{[V(I) + \sigma_\varepsilon^2 tr(AU)]^{1/2}\ [1 - \frac{2\sigma_\varepsilon^4 tr(AU)^2 + 4\sigma_\varepsilon^2 (a'AUAa)}{8[V(I) + \sigma_\varepsilon^2 tr(AU)]^2}]}$$

$$\{\ 1 + \frac{2\sigma_\varepsilon^2 tr(AU)^2 + 4\sigma_\varepsilon^2 (a'AUAa)}{4[V(I) + \sigma_\varepsilon^2 tr(AU)]^2\ [1 - \frac{2\sigma_\varepsilon^4 tr(AU)^2 + 4\sigma_\varepsilon^2 (a'AUAa)}{8[V(I) + \sigma_\varepsilon^2 tr(AU)]^2}]^2}$$

$$- \frac{\sigma_\varepsilon^2 [a'AUAa]}{V(I)[V(I) + \sigma_\varepsilon^2 tr(AU)]\ [1 - \frac{2\sigma_\varepsilon^4 tr(AU)^2 + 4\sigma_\varepsilon^2 (a'AUAa)}{8[V(I) + \sigma_\varepsilon^2 tr(AU)]^2}]}\ \} \quad (72a)$$

$$V[\Delta H|\hat{I}] \doteq \frac{[V(I)]^2}{[V(I) + \sigma_\varepsilon^2 tr(AU)]\ [1 - \frac{2\sigma_\varepsilon^4 tr(AU)^2 + 4\sigma_\varepsilon^2 (a'AUAa)}{8[V(I) + \sigma_\varepsilon^2 tr(AU)]^2}]^2}$$

$$\{\frac{\sigma_\varepsilon^2\ a'AUAa}{[V(I)]^2} + \frac{2\sigma_\varepsilon^4 tr(AU)^2 + 4\sigma_\varepsilon^2 (a'AUAa)}{4[V(I) + \sigma_\varepsilon^2 tr(AU)]^2\ [1 - \frac{2\sigma_\varepsilon^4 tr(AU)^2 + 4\sigma_\varepsilon^2 (a'AUAa)}{8[V(I) + \sigma_\varepsilon^2 tr(AU)]^2}]^2}$$

$$- \frac{2\sigma_\varepsilon^2\ a'AUAa}{V(I)\ [V(I) + \sigma_\varepsilon^2 tr(AU)]\ [1 - \frac{2\sigma_\varepsilon^4 tr(AU)^2 + \sigma_\varepsilon^2 (a'AUAa)}{8[V(I) + \sigma_\varepsilon^2 tr(AU)]^2}]}\} . \quad (72b)$$

(c) E[LRE] and V[LRE] are derived following the formulas 70a and 70b with the use of expressions 72a and 72b.

Because of the complexity of the approximate expressions, it seems almost impossible to assess the influence of the error variances by studying the equations. Therefore numerical values of these expressions were calculated, by substituting the proper values into formulas 71a, 71b, 72a and 72b. The results are given in Table 16. The substituted values depend on the characteristics of the selection index used, namely the genotypic variances and covariances, the economic weights and the variance-covariance matrix of the economic weights. For the selection index we used, the values were: $tr(AU) = 0.59627$, $tr(AU)^2 = 0.13907$, $a'AUAa = 0.36991$ and $V(I) = 1.1809$. When there is complete information (multiple

regression technique), matrix U has to be substituted by the $(X'X)^{-1}$ matrix from the multiple regression procedure and σ_ε^2 by the residual mean squares σ^2.

c. Discussion The β_1 and β_2 statistics calculated from the simulated samples indicate that $\Delta\hat{H}$, $\Delta H|\hat{I}$ and LRE are not normally distributed. To illustrate the shape, the distributions of $\Delta\hat{H}$, $\Delta H|\hat{I}$ and LRE are plotted in Figures 11 and 12.

The agreement between the numerical values obtained from the approximate equations and those from the Monte-Carlo simulation is not perfect. However, both series of estimates follow the same directional trends. The simulated and approximated numerical values of the expectations of $\Delta\hat{H}$, $\Delta H|\hat{I}$ and LRE, and of the variances of $\Delta H|\hat{I}$ agree reasonably well.

The discrepancy between the simulated variance estimates of $\Delta\hat{H}$ and LRE and those obtained by the approximate procedure are somewhat larger. The simulated variance estimates are consistently higher, and the differences tend to increase with increasing sampling variance (σ_ε^2) of the economic weight vector.

The discrepancies between the Monte-Carlo estimates and the results derived from the approximate equations may be caused by (1) the inaccuracies of the approximation technique (Taylor series) used in the development of expectations and variances, and (2) the sample size used in the Monte-Carlo process. The estimates are based on samples of 100 observations, which may be too small to comply with the assumption of selection in an infinite population.

The effects of random errors in the economic weight vector can be evaluated by looking at the biases of $\Delta\hat{H}$ and $\Delta H|\hat{I}$, at the expected relative

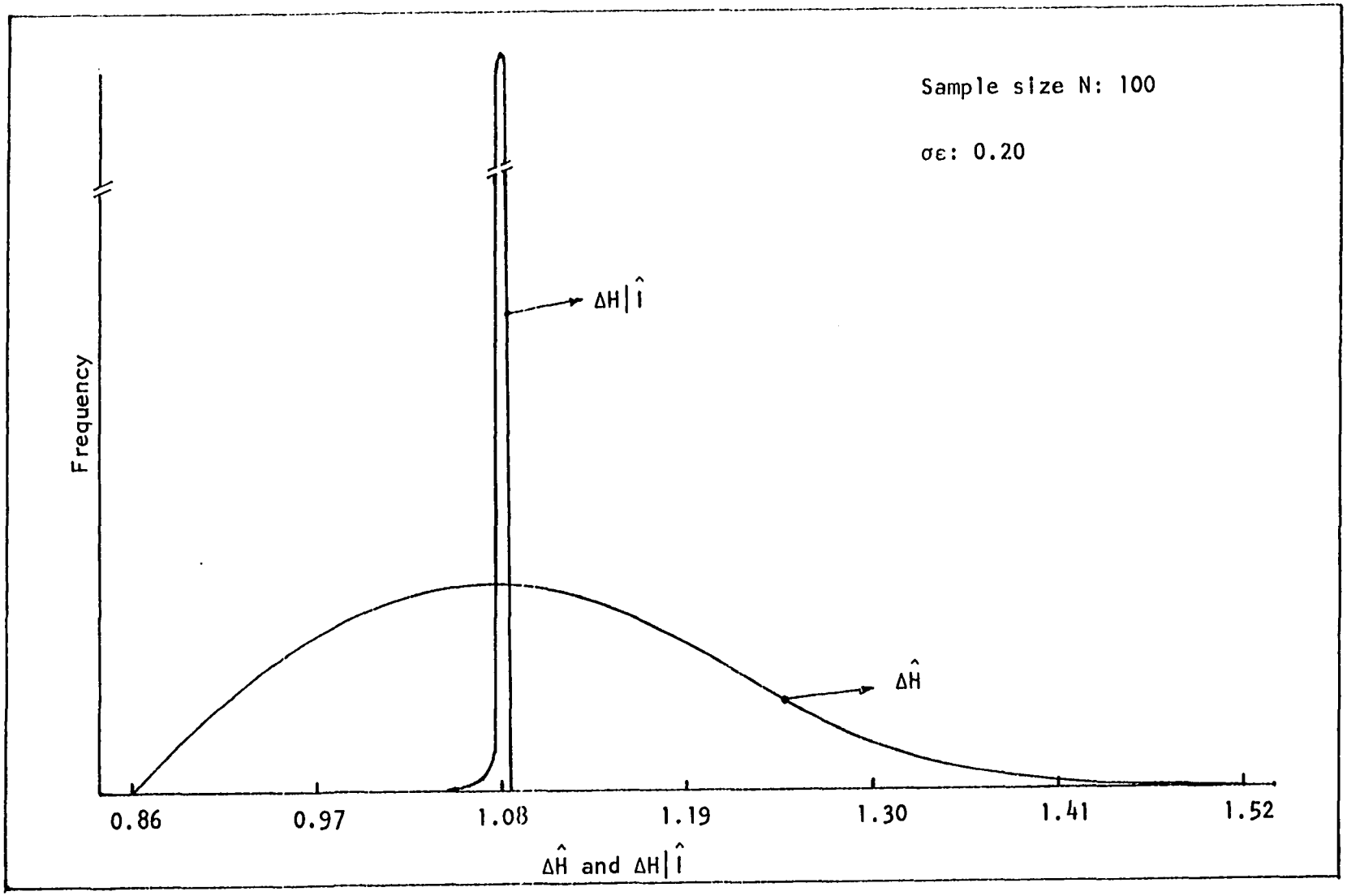


Figure 11. Distribution of $\Delta\hat{H}$ and $\Delta H|\hat{I}$

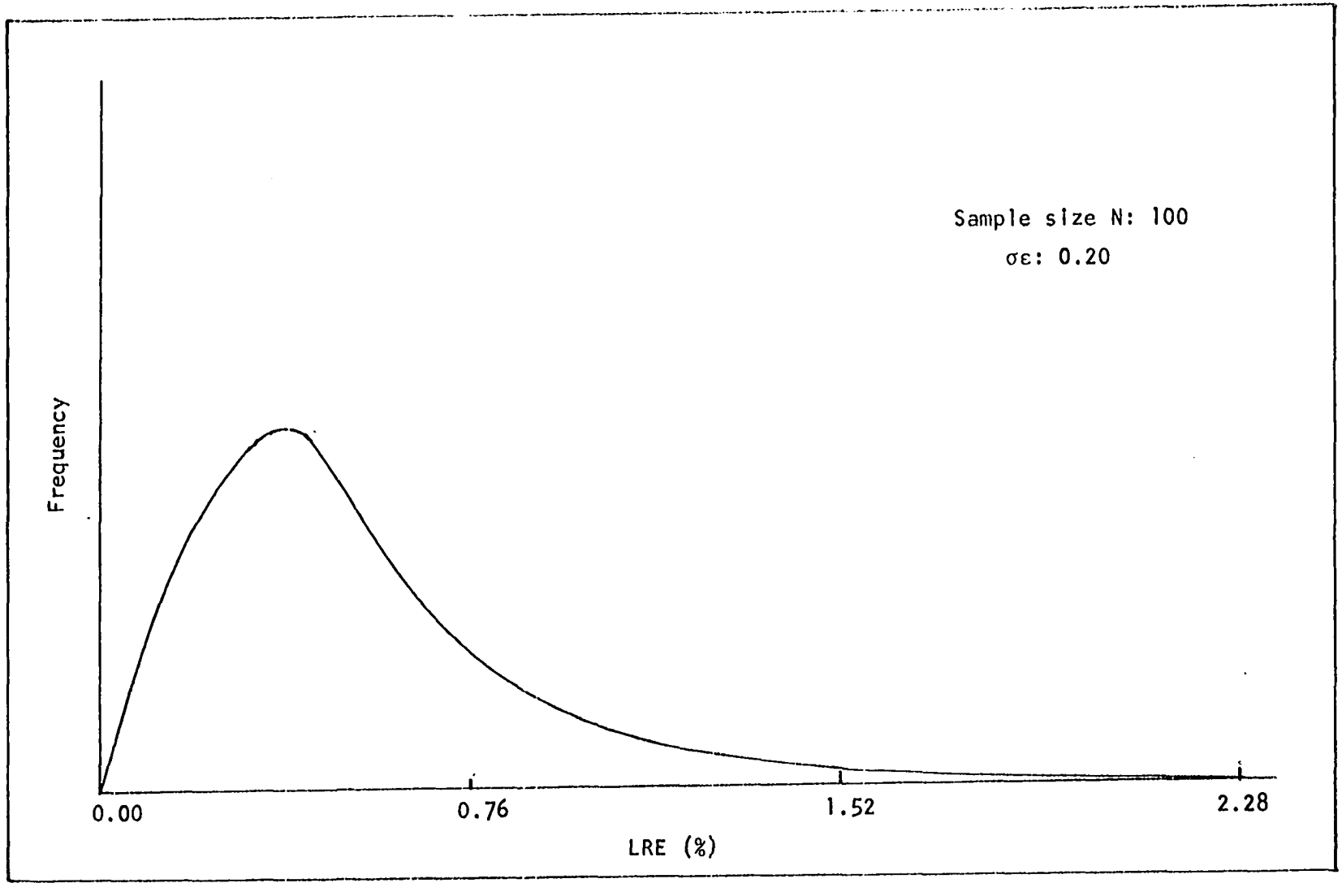


Figure 12. Distribution of LRE

efficiency and at the sampling variances of $\Delta\hat{H}$ and $\Delta H|\hat{I}$.

Three different relative biases can be calculated:

(a) $B1 = \dfrac{E(\Delta\hat{H}) - \Delta H}{\Delta H} \cdot 100$ measures with how much the estimated genetic gain $(\Delta\hat{H})$ overestimates the maximum attainable genetic gain (ΔH).

(b) $B2 = \dfrac{E(\Delta H|\hat{I}) - \Delta H}{\Delta H} \cdot 100$ measures the reduction in realized genetic gain $(\Delta H|\hat{I})$ relative to the maximum attainable genetic gain (ΔH).

(c) $B3 = \dfrac{E(\Delta\hat{H}) - E(\Delta H|\hat{I})}{E(\Delta H|\hat{I})} \cdot 100$ measures with how much the estimated genetic gain $(\Delta\hat{H})$ overestimates the realized genetic gain $E(\Delta H|\hat{I})$.

Estimates of B1, B2 and B3 for different sampling errors in the economic weight vector are listed in Table 17 and plotted in Figures 13 and 14.

The values of B1 and B2 indicate that $\Delta\hat{H}$ is an overestimate of ΔH by about the same amount as $\Delta H|\hat{I}$ is an underestimate of ΔH. This is illustrated in Figure 13, where B1 and B2 are almost symmetrical. For sampling errors (σ_ε) smaller than 0.5, the values of B1 and B2 are relatively small and approximately less than 1 percent. For larger sampling errors $(\sigma_\varepsilon = 1.0)$ the biases are considerable and the values of B1 and B2

Table 17. Relative bias of $\Delta\hat{H}$ and $\Delta H|\hat{I}$ estimates, and relative overestimation of realized genetic gain for different sampling errors in the economic weight vector

Sampling error (σ_ε)	B1 = $\frac{E(\Delta\hat{H}) - \Delta H}{\Delta H} \cdot 100$	B2 = $\frac{E(\Delta H\|\hat{I}) - \Delta H}{\Delta H} \cdot 100$	B3 = $\frac{E(\Delta\hat{H}) - E(\Delta H\|\hat{I})}{E(\Delta H\|\hat{I})} \cdot 100$
0.1	0.1197[a]	-0.1215	0.2413
	0.3819[b]	-0.1298	0.5123
0.2	0.4850	-0.4924	0.9821
	1.0206	-0.5108	1.5391
0.5	3.2190	-3.3864	6.8368
	4.5017	-3.3699	8.1461
1.0	14.1401	-14.9057	34.1335
	16.6072	-17.1759	40.7889

[a]Mathematically derived (approximation).

[b]Obtained by simulation.

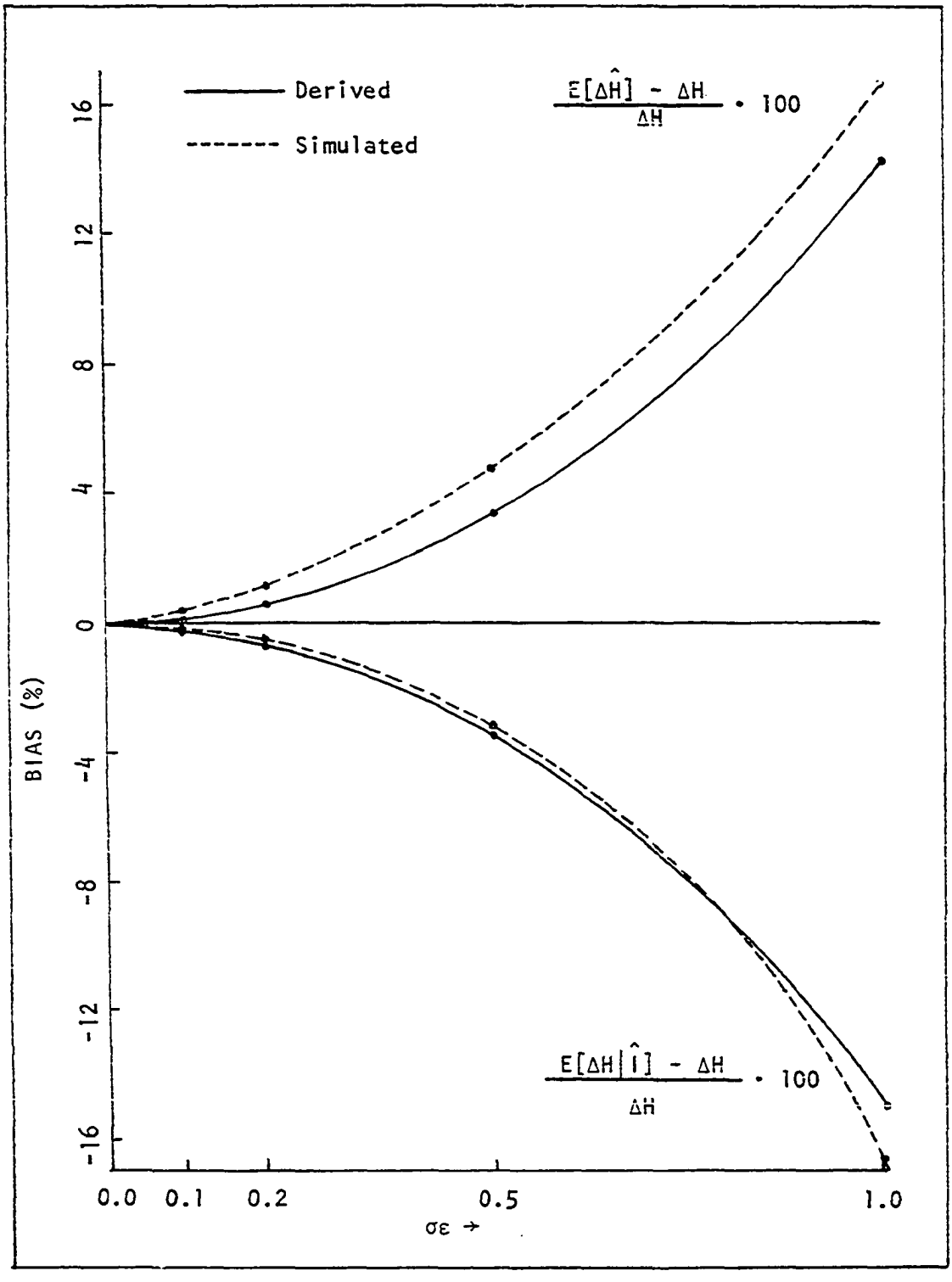


Figure 13. Relative bias of $\Delta\hat{H}$ and $\Delta H|\hat{I}$ estimates for different sampling errors in the economic weight vector

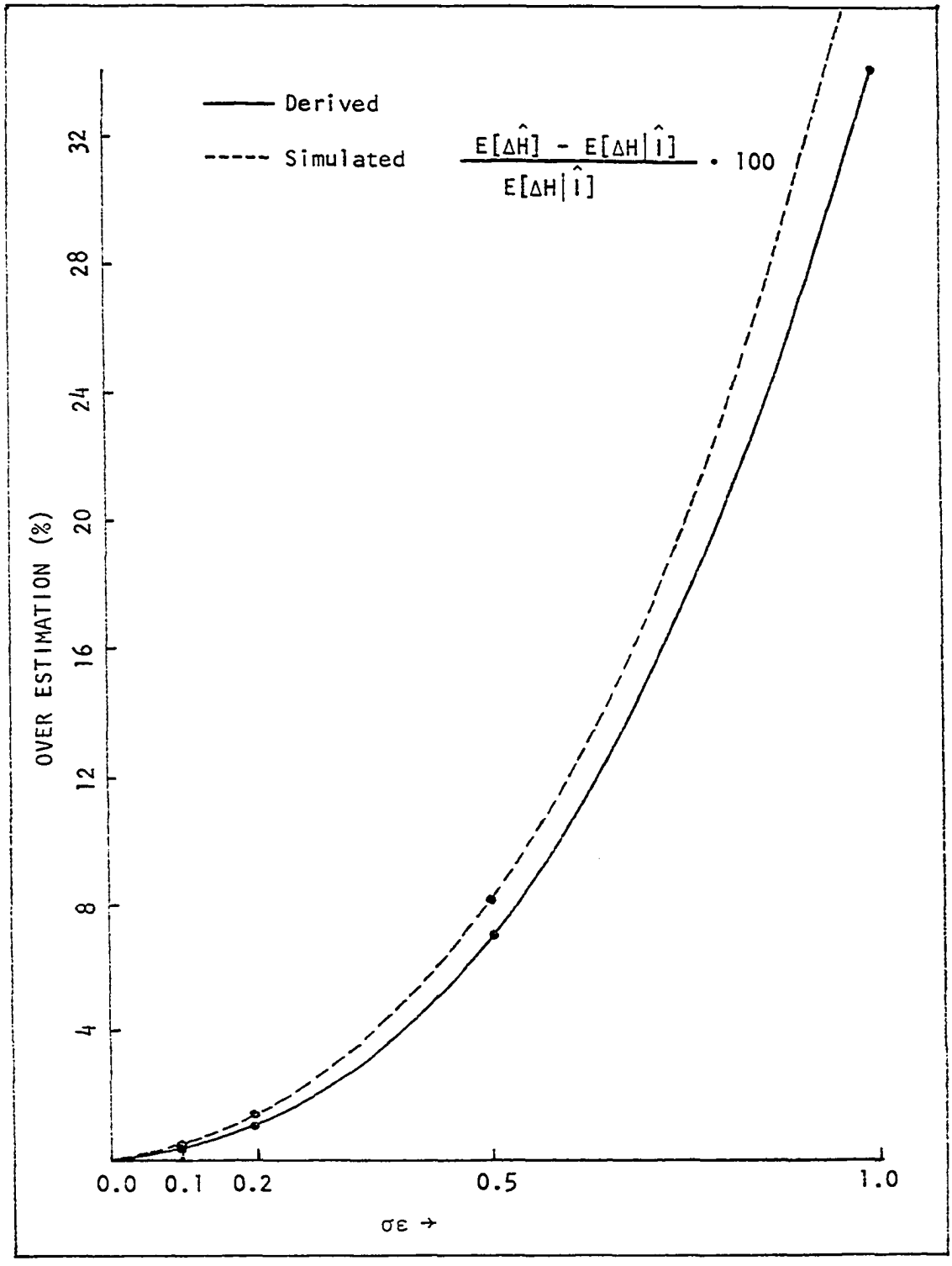


Figure 14. Relative overestimation of realized genetic gain for different sampling errors in the economic weight vector

are respectively 16.61 and -17.18 percent for the simulated estimates, and 14.14 and 14.90 percent for the derived estimates. The loss in relative efficiency (plotted in Figure 15) is approximately equal to B2 but with positive sign.

The effects of sampling errors in the economic weights on B3 (the relative overestimation of $\Delta H|\hat{I}$ by $\Delta\hat{H}$) are relatively small for small sampling errors, but fairly large for large sampling errors. For sampling errors of 0.2 the estimates for B3 are 0.98 percent (derived) and 1.54 percent (simulated), while for sampling errors of 1.0, B3 increases to 34.13 percent (derived) and 40.79 percent (simulated).

Because of the symmetry between B1 and B2 and the relationship between B2 and the loss in relative efficiency (LRE), the following rule of thumb can be used to get a rough idea about the bias of $\Delta\hat{H}$, $\Delta H|\hat{I}$ and the loss in relative efficiency, when the sampling errors in the economic weight vector are small.

$$\hat{\beta} = E(\Delta\hat{H}) - \Delta H$$

$$\doteq [V(I) + \sigma^2 tr(AU)]^{1/2} \left[1 - \frac{2\sigma^4 tr(AU)^2 + 4\sigma^2(a'AUAa)}{8[V(I) + \sigma^2 tr(AU)]^2}\right] - [V(I)]^{1/2}$$

where σ^2 = the residual mean square from the multiple regression procedure

$U = (X'X)^{-1}$ from the multiple regression procedure

$A = G'P^{-1}G$ from the selection index

a = the economic weight vector (multiple regression coefficients).

Then the estimates corrected for bias are approximate:

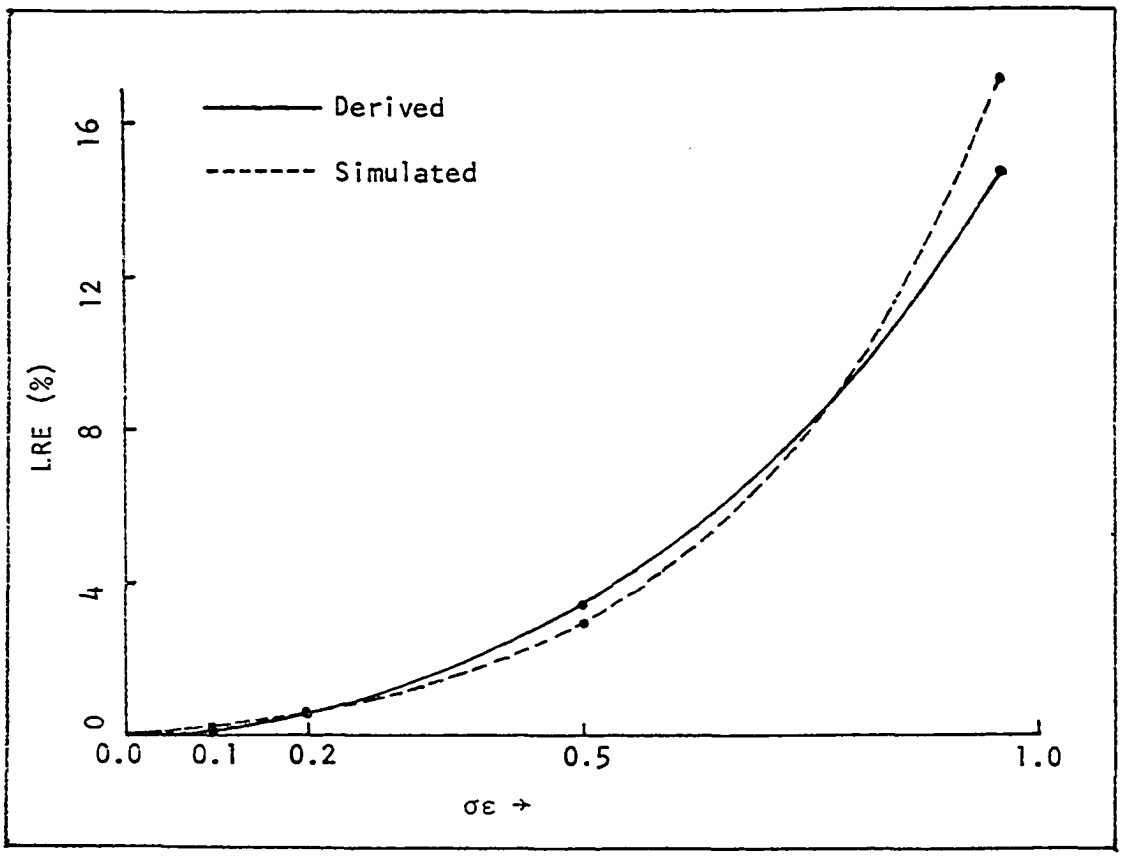


Figure 15. Loss in relative efficiency (LRE) for different sampling errors in the economic weight vector

$$\Delta H \doteq \Delta\hat{H} - \hat{\beta}$$

$$\Delta H|\hat{I} \doteq \Delta\hat{H} - 2\hat{\beta}$$

and the loss in relative efficiency

$$LRE \doteq \frac{\hat{\beta}}{\Delta H} \cdot 100 \ .$$

When the sampling variance is too large, the appropriate formulae should be used according to the expressions of B1, B2 and B3.

The variance of $\Delta\hat{H}$ and $\Delta H|\hat{I}$ for different sampling errors in the economic weight vector are given in Table 16 and plotted in Figure 16. The variance of $\Delta\hat{H}$ is relatively large and much larger than the variance of $\Delta H|\hat{I}$. Furthermore, increasing errors in the economic weight vector make the variance of ΔH increase at a much faster rate than the variance of $\Delta H|\hat{I}$. Since $\Delta\hat{H}$ is likely to have relatively large sampling errors we should be cautious not to draw far-reaching conclusions or to make derivations based on the value of $\Delta\hat{H}$.

A most important question for the animal breeder is the volume and kind of data which is sufficient to estimate the economic weights and to construct an adequate selection index. This will depend not only on the magnitude of the true parameters and the data available to estimate them, but also on the definition of an adequate selection index.

1) Data available For practical reasons pricing pigs on carcass quality has to be kept rather simple. However, the accuracy and the completeness of the data provided by the actual carcass grading procedures is sometimes questionable for the estimation of economic weights. In many instances grading is based on carcass weight, backfat thickness and

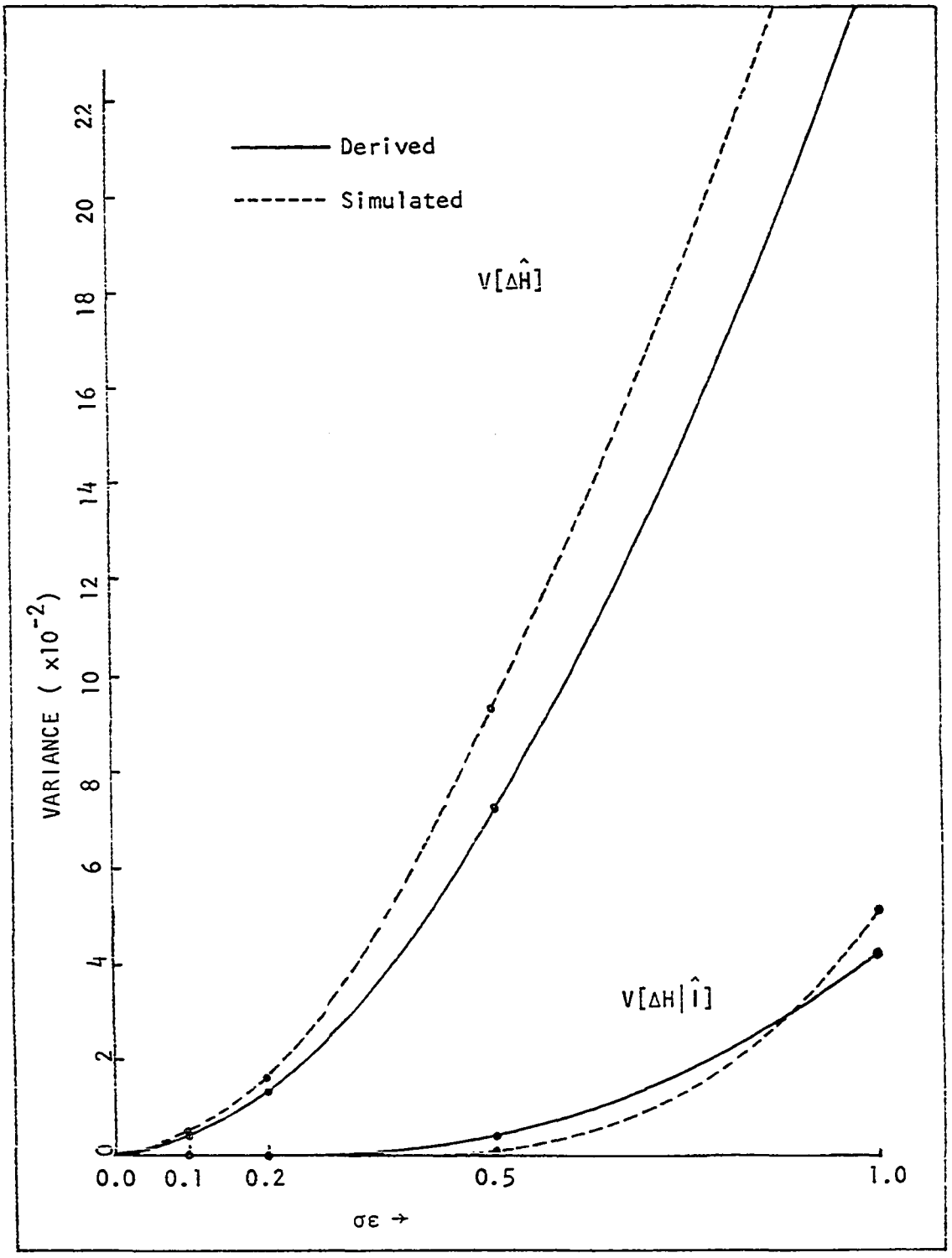


Figure 16. Variance of $\Delta\hat{H}$ and $\Delta H|\hat{I}$ for different sampling errors in the economic weight vector

a subjective meatiness score. But to what extent do these measures reflect monetary differences in carcass value? There is usually a considerable time lag between the grading system used in the industry and the ideas and criteria used by the animal breeders. Grading systems should be updated and reflect the true quality and value of the pig, because a good grading system is the best incentive for the industry to realize genetic change.

Sometimes the data will not be available to estimate the economic weights directly by multiple regression or if the data are available the regression may be very poor. In this case the short cut method (see Section III.B.) can be used. One might even consider eliminating traits such as loin-eye area because their economic weights are quasi-impossible to estimate accurately. Such traits could still be used in the index as an indirect measurement of percent ham and loin on the live pig.

2) An adequate selection index with respect to the economic weights This definition can be related to the following factors (a) the nearness of the expected gain from an index to the maximum possible gain or in other words the smallness of B1 and (b) the accuracy of predicting the gain from selection on the particular calculated index, or the smallness of B3.

We have tried to evaluate the effect of errors in single economic weights and sampling errors in the economic weight vector upon these criteria. The levels necessary for the satisfaction of these two criteria cannot be generally defined. Any answer to the question about the adequacy of a selection index will depend upon definitions, assumptions and

personal opinion. The answer to a particular situation shall be left to the reader. However, personally we feel that under the assumptions made, errors in single economic weights of less than 50 percent, and sampling errors (σ_ε) in the economic weight vector of less than 0.20 are not very critical.

This section can be concluded by stating that the loss in relative efficiency of a selection index and the biases and variances of $\Delta\hat{H}$ and $\Delta H|\hat{I}$ are function of:

(a) the sampling variances and covariances of the economic weights $\sigma^2(X'X)^{-1}$. This was studied by using different values for the sampling variance σ^2. When multiple regression procedures result in large residual mean squares (σ^2) or in a small multiple correlation coefficient R^2, the loss in relative efficiency of the resulting selection index can be large. The variances and biases of $\Delta\hat{H}$ and $\Delta H|\hat{I}$ can be considerable and make the estimates rather doubtful. However, when the sampling errors are small the resulting discrepancies are relatively unimportant.

(b) The magnitude of the $G'P^{-1}G$ matrix. This not only involves the genetic and phenotypic variances and covariances but also the number of traits in the aggregate genotype and index. Since this was not the real subject of our work, the genetic and phenotypic variances and covariances were considered as known constants, so that the effect of the $G'P^{-1}G$ matrix has not been studied.

D. Selection Indexes for a Nonlinear Aggregate Genotype

As mentioned previously a profit function or an aggregate genotype is not always linear in its variables. For the construction of the selection index that we used extensively in previous sections we have assumed a linear aggregate genotype by knowingly dropping the cross product terms. This was done to make the calculations and the interpretations less complicated. In this section we will consider a nonlinear aggregate genotype and calculate a quadratic index. Using an iterative procedure a linear approximation for the quadratic index will be calculated. The efficiency of this new linear index (calculated iteratively) and the one used previously will be calculated relative to the quadratic index.

1. Quadratic index

The construction of a quadratic selection index has been covered in section II.B subsection 2. The profit function (W) can be expressed by

$$W = R - C$$

where W = estimated profit per pig

R = gross return per pig

C = production cost per pig

When R and C are expressed in terms of the traits we want to select for, we obtain:

$$R = 205(0.766 + x_4)P$$

where 205 = average empty weight in pounds

0.766 = average dressing percent

x_4 = dressing percent as deviation from average

P = price per pound dressed.

$P = 0.30 - 0.0188x_3 + 0.0029x_5 + 0.0041x_6$ where

0.30 = price per pound dressed for average carcass

0.0188 = economic weight for backfat thickness (x_3)

0.0029 = economic weight for percent ham and loin (x_5)

0.0041 = economic weight for loin-eye area (x_6)

$C = K - 4.50x_1 + 5.80x_2 - 1.86x_7$

where 4.50 = economic weight for average daily gain (x_1)

5.80 = economic weight for feed efficiency (x_2)

1.86 = economic weight for average number of pigs weaned (x_7)

K = a constant corresponding to the cost of the average pig.

Notice that all variables x_i are expressed as deviations from the mean. After substituting R, P and C in W we obtain:

$$W = K' + 4.500x_1 - 5.800x_2 - 2,852x_3 + 0.6150x_4 + 0.4586x_5 + 0.5438x_6 + 1.8600x_7 - 0.0385x_3x_4 + 0.0059x_4x_5 + 0.0084x_4x_6 \quad (73)$$

where K' is a constant.

The cross product terms x_3x_4, x_4x_5 and x_4x_6 occur because of the interaction between dressing percent and backfat thickness, dressing percent and percent ham and loin, and dressing percent and loin-eye area, respectively.

After standardization and dropping of the constant term of expression (73) the aggregate genotype is

$$H = 0.7200g_1 - 1.4500g_2 - 0.4723g_3 + 1.0063g_4 + 0.8141g_5$$
$$+ 0.3971g_6 + 4.0518g_7 - \underline{0.0120g_3g_4}$$
$$+ \underline{0.0172g_4g_5} + \underline{0.0086g_4g_6} \quad . \qquad (74)$$

The only difference between this aggregate genotype and the one used previously is the occurrence of three cross products with appropriate economic weights.

The economic weights of the cross products are relatively small compared with the linear terms. This is an indication that the contribution of the cross products will be small.

The index coefficients for the quadratic index are obtained by solving the simultaneous equations. The solutions consisting of the B matrix (nonlinear part) and vector b (linear part) are given in Table 18. The quadratic index has 91 terms (13 linear terms, 12 squared terms and 66 cross products). The coefficients of the B matrix are relatively small. Although the calculation of a quadratic index is feasible, its operationality is questionable because of the complexity of the index.

2. Estimation of economic weights by iteration

The quadratic index will without doubt be the most efficient, because it makes maximum use of the information available. However, it is of some interest to know how the quadratic procedure can be changed to simplify the index without great reduction in relative efficiency. There are two possibilities: (a) to drop the nonlinear terms and (b) when the profit function is known, to estimate the economic weights iteratively so

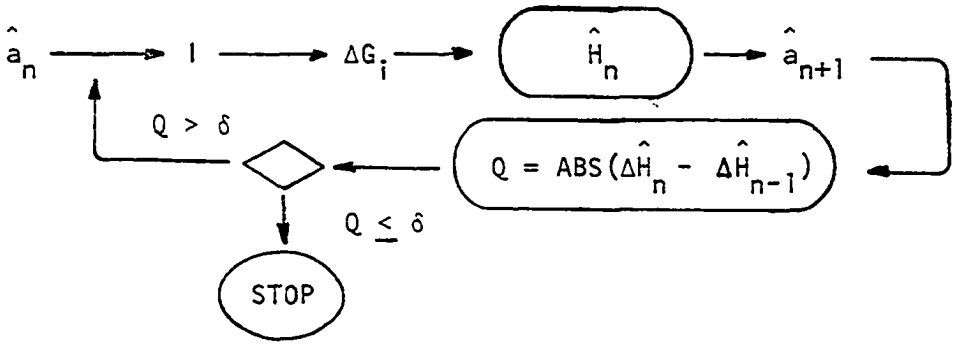
Table 18. Coefficients of the quadratic index ($x10^{-4}$)

Trait	1	2	3	4	5	6
	(a) B matrix ($x\ 10^{-4}$)					
1	5.080	11.390	7.298	1.862	2.060	1.060
2		6.381	8.502	2.078	2.298	1.246
3			-9.509	2.086	2.306	-3.426
4				0.159	0.352	0.324
5					0.195	0.358
6						-0.612
7						
8						
9						
10						
11						
12						
13						
	(b) b vector					
	-0.1400	-0.8168	-0.1637	-0.0241	-0.1589	-0.0144

7	8	9	10	11	12	13
0.612	-5.924	-9.026	-8.808	-3.200	-3.806	0.000
0.664	-6.500	-10.286	-10.056	-3.616	-4.400	0.000
2.162	-14.774	6.240	7.588	-0.082	-1.058	0.000
0.048	-0.760	-2.048	-2.044	-0.656	-0.770	0.000
0.066	-0.842	-2.262	-2.260	-0.726	-0.850	0.000
0.361	-2.436	1.254	1.482	0.054	-0.106	0.000
-0.042	0.388	-1.446	-1.518	-0.352	-0.358	0.000
	-0.554	10.798	11.168	2.840	3.034	0.000
		1.344	0.526	1.662	2.552	0.000
			-0.173	1.482	2.384	0.000
				0.798	1.068	0.000
					1.276	0.000
						0.000
-0.0359	0.1934	0.2357	0.2388	0.1668	-0.0661	0.2027

that the best linear approximation for the quadratic index can be calculated. The two procedures give indexes with 13 terms instead of 91 terms for the quadratic index.

The iterative scheme used was as follows:



Crude estimated economic weights ($\hat{a}_n$) for a linear aggregate genotype were used to calculate index I. Estimates for the genetic gains in the individual traits (ΔG_i) were calculated and passed through the aggregate genotype $\hat{H}$ one at a time and new economic weights (a_{n+1}) were estimated by $[\Delta\hat{H}/\Delta G_i]$, with g_j in expression (74) taking the value ΔG_i (i = 1,2,4,7) for i=j and zero otherwise, and by $[\Delta\hat{H}/\Delta G_i|G_4]$ with g_j taking the value G_i (i = 3,5,6) for i = j and zero otherwise. The absolute value of the difference between $\Delta\hat{H}_n$ and $\Delta\hat{H}_{n+1}$ (Q) was tested against δ. The iterative procedure was repeated until $Q \leq \delta$.

A stable solution was obtained after three iterations for $\delta = 10^{-7}$. The results are given in Table 19. Only the economic weights of traits 3 (backfat thickness), 5 (percent ham and loin) and 6 (loin-eye area) changed slightly.

Table 19. Economic weights, V(I), and V(H) when economic weights are estimated by iterative procedure

Iteration	Economic weights				
	1	2	3	4	5
1	0.719999	-1.49999	-0.471999	1.006299	0.813999
2	0.719999	-1.49999	-0.472958	1.006299	0.815210
3	0.719999	-1.49999	-0.472957	1.006299	0.815208

6	7	V(1)	V(H)	$\lvert \Delta\hat{H}_n - \Delta\hat{H}_{n+1} \rvert$
0.396999	4.054799	1.180881	4.902571	1.086683
0.397655	4.054799	1.182328	5.928555	0.000665
0.397654	4.054799	1.182328	5.928545	0.000000

3. Comparison of three selection indexes

The efficiency of the two linear indexes relative to the quadratic index have been calculated.

H_1 is the quadratic aggregate genotype.

I_1 is the quadratic index.

I_2 is the linear index calculated after dropping the nonlinear terms of the quadratic aggregate genotype.

I_3 is the linear index calculated as a linear approximation of the quadratic index. Its economic weights were calculated by an iterative procedure.

The efficiency of I_2 relative to I_1, is expressed by

$$\frac{R(I_2H_1)}{R(I_1H_1)} \times 100$$

and the relative efficiency of I_3 relative to I_1, is given by

$$\frac{R(I_3H_1)}{R(I_1H_1)} \times 100$$

The results are listed in Table 20.

The small difference in relative efficiency between the quadratic index I_1 and the linear indexes I_2 and I_3 can be explained by the small degree of nonlinearity in the aggregate genotype; there are only three cross products and their relative economic weights are small. The

Table 20. Comparison of three selection indexes

Index	V(I)	Rel. eff.
I_1	1.180890	100.000000
I_2	1.180882	99.999539
I_3	1.182328	99.999681

relative efficiencies are practically identical. However a linear index is preferred because of its greater simplicity.

The linear index calculated by iteration (I_3) is slightly more efficient than the linear index (I_2) (calculated after dropping the non-linear terms of the aggregate genotype). But the difference is practically too small to justify the iterative procedure. However under some circumstances (higher degree of nonlinearity) the iterative procedure could yield an index that is more efficient than the linear index derived without iteration.

V. SUMMARY AND CONCLUSIONS

A. Summary

Different selection indexes were calculated for the genetic improvement of pigs. By comparing their relative efficiencies the value of different sources of information was investigated.

Considering the cost of obtaining a piece of information to be included in a selection index and the contribution of that piece of information to the genetic change in a commercial population, an economic model was developed to estimate the net economic worth of different measurements. An example was worked out for an open and closed breeding structure.

The effects of errors in single economic weights on estimated genetic gain ($\Delta\hat{H}$), realized genetic gain ($\Delta H|\hat{I}$) and the loss in relative efficiency (LRE) were evaluated.

The effects of simultaneous errors in the economic weight vector were studied. Monte-Carlo simulation and the Taylor series expansion technique were used to calculate expectations and variances of $\Delta\hat{H}$ and $\Delta H|\hat{I}$. Biases and the loss in relative efficiency were calculated for errors of different magnitudes.

By estimating the economic weights iteratively, a linear approximation of a quadratic index was obtained. The efficiences of a straight linear index and the linear approximate index were calculated relative to the quadratic index.

B. Conclusions

When the testing capacity is limited and selection intensity considered, including carcass information of sibs in a selection index reduces the relative efficiency of a selection procedure by 35 to 45 percent depending upon the selection indexes used. Including carcass information of sibs in a selection index is economically not justified. However, the increasing problems with PSS (Porcine Stress Syndrome) and PSE (Pale, Soft and Exudative) meat have to be considered before basing all selection on the performance of boars only. The finding of an operational and nondetrimental PSE sensibility test for live pigs could help solve this problem more efficiently than examining carcasses of sibs.

Under the assumptions made, measuring individual feed efficiency of the boars as compared with pen feed efficiency is only economically justified when a multipler system is introduced.

When the same genetic and phenotypic parameters for ultrasonic (US) loin-eye measurement are assumed as for carcass loin-eye measurement, the use of the individual US loin-eye instead of carcass information on sibs results in a selection index with three percent greater efficiency. Considering the selection intensity the total selection procedure is 38 to 48 percent more efficient. This suggests that the search should be intensified for better carcass evaluation methods on live animals.

Errors in single economic weights can result in considerable bias in the estimated gain ($\hat{\Delta H}$). Moderate errors (from minus 50 percent to

plus 50 percent) have relatively small effects on real genetic gain ($\Delta H|\hat{I}$); the loss in relative efficiency over this range is less than 1 percent. The effects of errors in single economic weights are non-linear and nonsymmetrical Negative errors (under estimation) are in general more critical than positive errors (over estimation). The effects of errors in single economic weights depend on the relative economic importance of the trait, the heritability and the variance covariance structure.

Results obtained by Monte-Carlo simulation indicate that $\hat{\Delta H}$, $\Delta H|\hat{I}$ and LRE are not normally distributed. The agreement between the numerical values obtained from the derived approximate equations and those from the Monte-Carlo simulation is not perfect but reasonably good for $E(\hat{\Delta H})$, $E(\Delta H|\hat{I})$, E(LRE) and $V(\Delta H|\hat{I})$. The discrepancy between the derived and the simulated estimates of $V(\hat{\Delta H})$ and V(LRE) are somewhat larger. The simulated estimates are consistently higher and the difference tends to increase with increasing sampling errors (σ_e).

The loss in relative efficiency and the relative biases of $\hat{\Delta H}$ and $\Delta H|\hat{I}$ are roughly of the same magnitude. The relative biases of $\hat{\Delta H}$ and $\Delta H|\hat{I}$ are opposite in sign; $\hat{\Delta H}$ is an overestimate of ΔH, while $\Delta H|\hat{I}$ is an underestimate of ΔH. Under the assumptions made and for small sampling errors in the economic weight vector ($\sigma_e < 0.50$) the loss in relative efficiency is less than 2.6 percent but increases to approximately 15 percent for $\sigma_e = 1.0$. For relatively small sampling errors in the economic weight vector ($\sigma_e < 0.20$), the relative biases in $\hat{\Delta H}$ and $\Delta H|\hat{I}$ are less than 1 percent. For large sampling errors ($\sigma_e = 1.0$) the biases of $\hat{\Delta H}$

and $\Delta H|\hat{I}$ are considerable, namely 16.61 and -17.18 percent for the simulated estimates, and 14.14 and 14.90 percent for the derived estimates, respectively.

The difference between realized genetic gain ($\Delta H|\hat{I}$) and estimated genetic gain ($\hat{\Delta H}$) is small for small sampling errors but becomes fairly large for large sampling errors. For sampling errors of $\sigma_\epsilon = 0.20$, the latter is 0.98 percent (derived) and 1.54 percent (simulated), while for sampling errors of $\sigma_\epsilon = 1.00$, the relative over estimation increases to 34.14 percent (derived) and 40.79 percent (simulated).

The variance of $\hat{\Delta H}$ is relatively large and much larger than the variance of $\Delta H|\hat{I}$. Furthermore, increasing sampling errors in the economic weight vector make the variance of $\hat{\Delta H}$ increase at a much faster rate than the variance of $\Delta H|\hat{I}$. Because of the likelihood of large sampling errors in $\hat{\Delta H}$ we must be cautious when far-reaching conclusions and derivations are based on estimates of $\hat{\Delta H}$.

For moderate sampling errors in the economic weight vector these preliminary results are a strong argument for the robustness of the selection index theory. However, more research is needed in this field to be conclusive. The final goal should be to calculate confidence limits for $\hat{\Delta H}$ and $\Delta H|\hat{I}$ in terms of the error structure of the parameters involved. This is a rather complicated matter because it involves not only the economic weights, but also simultaneously heritabilitily estimates and estimates of genetic and phenotypic correlations and the joint sampling distribution of all these estimates. This can only be

accomplished by (a) searching for better ways to evaluate expectations and variances of complex functions, and (b) finding realistic approximations for the density functions of $\Delta\hat{H}$ and $\Delta H|\hat{I}$ in terms of the error structure of the parameters involved.

A quadratic index was calculated. The difference in efficiency as compared with a straight linear index was negligible, and the quadratic index was too complex for practical purposes. By calculating the economic weights iteratively a new index was calculated as a linear approximation of the quadratic index. The degree of nonlinearity in the aggregate genotype was too small to show significant differences in relative efficiency. However the results indicate that under some circumstances (extreme nonlinearity) the iterative procedure could yield an index that is more efficient than a straight linear index and less complex than a quadratic index.

VI. LITERATURE CITED

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VIII. APPENDIX A: CALCULATED INDEXES

INDEX 1 : COMPLETE INDEX

	VARIATE		B-VALUE	VALUE OF VARIATE (1)
1	AV.D.GAIN	(B1)	-0.1400	0.3513
2	FEED EFF.	(B1)	-0.8168	11.1611
3	B.FAT(PROBE)	(B1)	-0.1637	0.6414
4	AV.D.GAIN	(B2)	-0.0241	0.0104
5	FEED EFF.	(B2)	-0.1589	0.3996
6	B.FAT(PROBE)	(B2)	-0.0144	0.0049
7	AV.B.FAT(CARC.)	(H+G)	-0.0359	0.0194
8	AV.DRESSING %	(H+G)	0.1934	0.7270
9	AV.% HAM+LOIN	(H+G)	0.2357	0.8036
10	AV. LOIN-EYE	(H+G)	0.2388	1.1223
11	AV.D.GAIN	(H+G)	0.1668	0.2509
12	AV.FEED EFF.	(H+G)	-0.0661	0.0336
13	AV. # WEANED		0.2027	1.7560

VARIANCE OF INDEX 1.1809
STD DEV OF INDEX 1.0867

VARIANCE OF AGG GENOT 4.9026
STD DEV OF AGG GENOT 2.2142

CORRELATION OF INDEX AND AGG GENOT 0.4908

REGRESSION OF EACH TRAIT ON INDEX, CORRELATION OF EACH TRAIT WITH INDEX, PERCENT OF ECONOMIC GAINS (2)

	TRAIT	REGRESSION	CORRELATION	PCT OF GAIN
1	AV.D.GAIN	0.1283	0.2546	9.2381
2	FEED EFF.	-0.3099	-0.5692	44.9327
3	B.FAT(CARCASS)	-0.2234	-0.3619	10.5445
4	DRESSING %	0.0702	0.1392	7.0587
5	% HAM + LOIN	0.2241	0.3630	18.2386
6	LOIN-EYE	0.1639	0.2401	6.5064
7	AV.#WEANED	0.0086	0.0295	3.4811

(1) VALUE OF EACH VARIATE IN THE INDEX IS PERCENT REDUCTION IN RATE OF OVERALL GENETIC GAIN IF THAT VARIATE IS OMITTED
(2) THESE FIGURES ARE THE PERCENTAGES OF TOTAL GAIN ACCOUNTED FOR BY GAIN IN EACH TRAIT

INDEX 2 : NUMBER WEANED DELETED FROM COMPLETE INDEX

	VARIATE		B-VALUE	VALUE OF VARIATE (1)
1	AV.D.GAIN	(B1)	-0.1400	0.3640
2	FEED EFF.	(B1)	-0.8168	11.5900
3	B.FAT(PROBE)	(B1)	-0.1637	0.6646
4	AV.D.GAIN	(B2)	-0.0241	0.0108
5	FEED EFF.	(B2)	-0.1589	0.4140
6	B.FAT(PROBE)	(B2)	-0.0144	0.0051
7	AV.B.FAT(CARC.)	(H+G)	-0.0359	0.0201
8	AV.DRESSING %	(H+G)	0.1934	0.7533
9	AV.% HAM+LOIN	(H+G)	0.2357	0.8327
10	AV. LOIN-EYE	(H+G)	0.2388	1.1630
11	AV.D.GAIN	(H+G)	0.1668	0.2599
12	AV.FEED EFF.	(H+G)	-0.0661	0.0349

VARIANCE OF INDEX 1.1398
STD DEV OF INDEX 1.0676

VARIANCE OF AGG GENOT 4.9026
STD DEV OF AGG GENOT 2.2142

CORRELATION OF INDEX AND AGG GENOT 0.4822

REGRESSION OF EACH TRAIT ON INDEX, CORRELATION OF EACH TRAIT WITH INDEX, PERCENT OF ECONOMIC GAINS (2)

	TRAIT	REGRESSION	CORRELATION	PCT OF GAIN
1	AV.D.GAIN	0.1329	0.2591	9.5713
2	FEED EFF.	-0.3211	-0.5794	46.5533
3	B.FAT(CARCASS)	-0.2315	-0.3684	10.9248
4	DRESSING %	0.0727	0.1417	7.3132
5	% HAM + LOIN	0.2321	0.3695	18.8963
6	LOIN-EYE	0.1698	0.2444	6.7411
7	AV.#WEANED	0.0	0.0	0.0

(1) VALUE OF EACH VARIATE IN THE INDEX IS PERCENT REDUCTION IN RATE OF OVERALL GENETIC GAIN IF THAT VARIATE IS OMITTED
(2) THESE FIGURES ARE THE PERCENTAGES OF TOTAL GAIN ACCOUNTED FOR BY GAIN IN EACH TRAIT

INDEX 3 : INDIVIDUAL FEED EFF. OF THE BOARS SUBSTITUTED BY THE BOAR PEN FEED EFF.

	VARIATE		B-VALUE	VALUE OF VARIATE (1)
1	AV.D.GAIN	(B1)	0.0775	0.1598
2	B.FAT(PROBE)	(B1)	-0.3130	3.0743
3	AV.D.GAIN	(B2)	-0.2383	1.5194
4	B.FAT(PROBE)	(B2)	0.1329	0.5473
5	AV.FEED EFF.	(B1+B2)	-0.9710	9.8596
6	AV.B.FAT(CARC.)	(H+G)	-0.0354	0.0201
7	AV.DRESSING %	(H+G)	0.1936	0.7764
8	AV.% HAM+LOIN	(H+G)	0.2360	0.8579
9	AV. LOIN-EYE	(H+G)	0.2389	1.1970
10	AV.D.GAIN	(H+G)	0.1662	0.2655
11	AV.FEED EFF.	(H+G)	-0.0673	0.0371
12	AV. # WEANED		0.2027	1.8717

VARIANCE OF INDEX 1.1085
STD DEV OF INDEX 1.0529

VARIANCE OF AGG GENOT 4.9026
STD DEV OF AGG GENOT 2.2142

CORRELATION OF INDEX AND AGG GENOT 0.4755

REGRESSION OF EACH TRAIT ON INDEX, CORRELATION OF EACH TRAIT WITH INDEX, PERCENT OF ECONOMIC GAINS (2)

	TRAIT	REGRESSION	CORRELATION	PCT OF GAIN
1	AV.D.GAIN	0.1275	0.2450	9.1766
2	FEED EFF.	-0.3091	-0.5501	44.8171
3	B.FAT(CARCASS)	-0.2399	-0.3765	11.3210
4	DRESSING %	0.0598	0.1149	6.0113
5	% HAM + LOIN	0.2236	0.3509	18.2012
6	LOIN-EYE	0.1704	0.2419	6.7644
7	AV.#WEANED	0.0091	0.0304	3.7083

(1) VALUE OF EACH VARIATE IN THE INDEX IS PERCENT REDUCTION IN RATE OF OVERALL GENETIC GAIN IF THAT VARIATE IS OMITTED
(2) THESE FIGURES ARE THE PERCENTAGES OF TOTAL GAIN ACCOUNTED FOR BY GAIN IN EACH TRAIT

INDEX 4 : AV. DRESSING PERCENT DELETED FRCM COMPLETE INDEX

	VARIATE		B-VALUE	VALUE OF VARIATE (1)
1	AV.D.GAIN	(B1)	-0.1494	0.4075
2	FEED EFF.	(B1)	-0.8256	11.6192
3	B.FAT(PROBE)	(B1)	-0.1576	0.6039
4	AV.D.GAIN	(B2)	-0.0336	0.0205
5	FEED EFF.	(B2)	-0.1677	0.4527
6	B.FAT(PROBE)	(B2)	-0.0083	0.0017
7	AV.B.FAT(CARC.)	(H+G)	0.0400	0.0279
8	AV.% HAM+LOIN	(H+G)	0.2064	0.6356
9	AV. LOIN-EYE	(H+G)	0.2876	1.7722
10	AV.D.GAIN	(H+G)	0.0647	0.0440
11	AV.FEED EFF.	(H+G)	-0.1892	0.3332
12	AV. # WEANED		0.2027	1.7820

VARIANCE OF INDEX 1.1638
STD DEV OF INDEX 1.0788

VARIANCE OF AGG GENOT 4.9026
STD DEV OF AGG GENOT 2.2142

CORRELATION OF INDEX AND AGG GENOT 0.4872

REGRESSION OF EACH TRAIT ON INDEX, CORRELATION OF EACH TRAIT WITH INDEX, PERCENT OF ECONOMIC GAINS (2)

	TRAIT	REGRESSION	CORRELATION	PCT OF GAIN
1	AV.D.GAIN	0.1327	0.2613	9.5533
2	FEED EFF.	-0.3140	-0.5725	45.5252
3	B.FAT(CARCASS)	-0.2263	-0.3639	10.6797
4	DRESSING %	0.0546	0.1075	5.4914
5	% HAM + LOIN	0.2277	0.3661	18.5330
6	LOIN-EYE	0.1684	0.2450	6.6852
7	AV.#WEANED	0.0087	0.0297	3.5323

(1) VALUE OF EACH VARIATE IN THE INDEX IS PERCENT REDUCTION IN RATE OF OVERALL GENETIC GAIN IF THAT VARIATE IS OMITTED
(2) THESE FIGURES ARE THE PERCENTAGES OF TOTAL GAIN ACCOUNTED FOR BY GAIN IN EACH TRAIT

INDEX 5 : AV. DRESSING PERCENT AND NUMBER WEANED DELETED FROM COMPLETE INDEX

	VARIATE		B-VALUE	VALUE OF VARIATE (1)
1	AV.D.GAIN	(B1)	-0.1494	0.4225
2	FEED EFF.	(B1)	-0.8256	12.0738
3	B.FAT(PROBE)	(B1)	-0.1576	0.6261
4	AV.D.GAIN	(B2)	-0.0336	0.0213
5	FEED EFF.	(B2)	-0.1677	0.4693
6	B.FAT(PROBE)	(B2)	-0.0083	0.0018
7	AV.B.FAT(CARC.)	(H+G)	0.0400	0.0289
8	AV.% HAM+LOIN	(H+G)	0.2064	0.6590
9	AV. LOIN-EYE	(H+G)	0.2876	1.8377
10	AV.D.GAIN	(H+G)	0.0647	0.0456
11	AV.FEED EFF.	(H+G)	-0.1892	0.3454

VARIANCE OF INDEX 1.1227
STD DEV OF INDEX 1.0596

VARIANCE OF AGG GENOT 4.9026
STD DEV OF AGG GENOT 2.2142

CORRELATION OF INDEX AND AGG GENOT 0.4785

REGRESSION OF EACH TRAIT ON INDEX, CORRELATION OF EACH TRAIT WITH INDEX, PERCENT OF ECONOMIC GAINS (2)

	TRAIT	REGRESSION	CORRELATION	PCT OF GAIN
1	AV.D.GAIN	0.1375	0.2661	9.9032
2	FEED EFF.	-0.3255	-0.5829	47.1921
3	B.FAT(CARCASS)	-0.2345	-0.3705	11.0707
4	DRESSING %	0.0566	0.1095	5.6924
5	% HAM + LOIN	0.2360	0.3728	19.2116
6	LOIN-EYE	0.1746	0.2494	6.9300
7	AV.#WEANED	0.0	0.0	0.0

(1) VALUE OF EACH VARIATE IN THE INDEX IS PERCENT REDUCTION IN RATE OF OVERALL GENETIC GAIN IF THAT VARIATE IS OMITTED
(2) THESE FIGURES ARE THE PERCENTAGES OF TOTAL GAIN ACCOUNTED FOR BY GAIN IN EACH TRAIT

INDEX 6 : AV. FEED EFF. AND AV. DAILY GAIN OF SIBS DELETED FROM COMPLETE INDEX

	VARIATE		B-VALUE	VALUE OF VARIATE (1)
1	AV.D.GAIN	(B1)	-0.1120	0.2351
2	FEED EFF.	(B1)	-0.8380	12.3816
3	B.FAT(PROBE)	(B1)	-0.1586	0.6152
4	AV.D.GAIN	(B2)	0.0039	0.0003
5	FEED EFF.	(B2)	-0.1801	0.5381
6	B.FAT(PROBE)	(B2)	-0.0093	0.0021
7	AV.B.FAT(CARC.)	(H+G)	-0.0425	0.0336
8	AV.DRESSING %	(H+G)	0.1912	0.8723
9	AV.% HAM+LOIN	(H+G)	0.2333	0.9915
10	AV. LOIN-EYE	(H+G)	0.2294	1.1064
11	AV. # WEANED		0.2027	1.7925

VARIANCE OF INDEX 1.1570
STD DEV OF INDEX 1.0757

VARIANCE OF AGG GENOT 4.9026
STD DEV OF AGG GENOT 2.2142

CORRELATION OF INDEX AND AGG GENOT 0.4858

REGRESSION OF EACH TRAIT ON INDEX, CORRELATION OF EACH TRAIT WITH INDEX, PERCENT OF ECONOMIC GAINS (2)

	TRAIT	REGRESSION	CORRELATION	PCT OF GAIN
1	AV.D.GAIN	0.1207	0.2370	8.6880
2	FEED EFF.	-0.3071	-0.5583	44.5238
3	B.FAT(CARCASS)	-0.2273	-0.3645	10.7302
4	DRESSING %	0.0724	0.1423	7.2872
5	% HAM + LOIN	0.2287	0.3668	18.6200
6	LOIN-EYE	0.1662	0.2411	6.5980
7	AV.#WEANED	0.0088	0.0298	3.5528

(1) VALUE OF EACH VARIATE IN THE INDEX IS PERCENT REDUCTION IN RATE OF OVERALL GENETIC GAIN IF THAT VARIATE IS OMITTED
(2) THESE FIGURES ARE THE PERCENTAGES OF TOTAL GAIN ACCOUNTED FOR BY GAIN IN EACH TRAIT

INDEX 7 : ALL SIB INFORMATION DELETED FROM COMPLETE INDEX

	VARIATE		B-VALUE	VALUE OF VARIATE (1)
1	AV.D.GAIN	(B1)	-0.1890	0.7880
2	FEED EFF.	(B1)	-0.9227	18.2671
3	B.FAT(PROBE)	(B1)	-0.1551	0.7186
4	AV.D.GAIN	(B2)	-0.0731	0.1175
5	FEED EFF.	(B2)	-0.2648	1.3763
6	B.FAT(PROBE)	(B2)	-0.0058	0.0010
7	AV. # WEANED		0.2027	2.0550

VARIANCE OF INDEX 1.0106
STD DEV OF INDEX 1.0053

VARIANCE OF AGG GENOT 4.9026
STD DEV OF AGG GENOT 2.2142

CORRELATION OF INDEX AND AGG GENOT 0.4540

REGRESSION OF EACH TRAIT ON INDEX, CORRELATION OF EACH TRAIT WITH INDEX, PERCENT OF ECONOMIC GAINS (2)

	TRAIT	REGRESSION	CORRELATION	PCT OF GAIN
1	AV.D.GAIN	0.1521	0.2791	10.9506
2	FEED EFF.	-0.3396	-0.5770	49.2389
3	B.FAT(CARCASS)	-0.2390	-0.3582	11.2818
4	DRESSING %	0.0502	0.0921	5.0489
5	% HAM + LOIN	0.1915	0.2870	15.5911
6	LOIN-EYE	0.0962	0.1305	3.8207
7	AV.#WEANED	0.0100	0.0319	4.0678

(1) VALUE OF EACH VARIATE IN THE INDEX IS PERCENT REDUCTION IN RATE OF OVERALL GENETIC GAIN IF THAT VARIATE IS OMITTED
(2) THESE FIGURES ARE THE PERCENTAGES OF TOTAL GAIN ACCOUNTED FOR BY GAIN IN EACH TRAIT

INDEX 8 : ALL SIB INFORMATION AND NUMBER WEANED DELETED FROM COMPLETE INDEX

	VARIATE		B-VALUE	VALUE OF VARIATE (1)
1	AV.D.GAIN	(B1)	-0.1890	0.8216
2	FEED EFF.	(B1)	-0.9227	19.1328
3	B.FAT(PROBE)	(B1)	-0.1551	0.7492
4	AV.D.GAIN	(B2)	-0.0731	0.1224
5	FEED EFF.	(B2)	-0.2648	1.4351
6	B.FAT(PROBE)	(B2)	-0.0058	0.0010

VARIANCE OF INDEX 0.9694
STD DEV OF INDEX 0.9846

VARIANCE OF AGG GENOT 4.9026
STD DEV OF AGG GENOT 2.2142

CORRELATION OF INDEX AND AGG GENOT 0.4447

REGRESSION OF EACH TRAIT ON INDEX, CORRELATION OF EACH TRAIT WITH INDEX, PERCENT OF ECONOMIC GAINS (2)

	TRAIT	REGRESSION	CORRELATION	PCT OF GAIN
1	AV.D.GAIN	0.1585	0.2850	11.4149
2	FEED EFF.	-0.3540	-0.5891	51.3268
3	B.FAT(CARCASS)	-0.2492	-0.3657	11.7602
4	DRESSING %	0.0523	0.0940	5.2630
5	% HAM + LOIN	0.1997	0.2931	16.2522
6	LOIN-EYE	0.1003	0.1332	3.9828
7	AV.#WEANED	0.0	0.0	0.0

(1) VALUE OF EACH VARIATE IN THE INDEX IS PERCENT REDUCTION IN RATE OF OVERALL GENETIC GAIN IF THAT VARIATE IS OMITTED
(2) THESE FIGURES ARE THE PERCENTAGES OF TOTAL GAIN ACCOUNTED FOR BY GAIN IN EACH TRAIT

INDEX 9 : ALL CARCASS INFORMATION OF SIBS DELETED FROM THE COMPLETE INDEX

	VARIATE		B-VALUE	VALUE OF VARIATE (1)
1	AV.D.GAIN	(B1)	-0.1734	0.6066
2	FEED EFF.	(B1)	-0.8492	13.7619
3	B.FAT(PROBE)	(B1)	-0.1469	0.6107
4	AV.D.GAIN	(B2)	-0.0575	0.0666
5	FEED EFF.	(B2)	-0.1913	0.6524
6	B.FAT(PROBE)	(B2)	0.0024	0.0002
7	AV.D.GAIN	(H+G)	-0.1131	0.1945
8	AV.FEED EFF.	(H+G)	-0.3803	2.1982
9	AV. # WEANED		0.2027	1.9499

VARIANCE OF INDEX 1.0645
STD DEV OF INDEX 1.0317

VARIANCE OF AGG GENOT 4.9026
STD DEV OF AGG GENOT 2.2142

CORRELATION OF INDEX AND AGG GENOT 0.4660

REGRESSION OF EACH TRAIT ON INDEX, CORRELATION OF EACH TRAIT WITH INDEX, PERCENT OF ECONOMIC GAINS (2)

	TRAIT	REGRESSION	CORRELATION	PCT OF GAIN
1	AV.D.GAIN	0.1523	0.2869	10.9666
2	FEED EFF.	-0.3401	-0.5931	49.3115
3	B.FAT(CARCASS)	-0.2347	-0.3610	11.0778
4	DRESSING %	0.0530	0.0999	5.3366
5	% HAM + LOIN	0.1922	0.2957	15.6482
6	LOIN-EYE	0.0957	0.1331	3.7976
7	AV.#WEANED	0.0095	0.0311	3.8618

(1) VALUE OF EACH VARIATE IN THE INDEX IS PERCENT REDUCTION IN RATE OF OVERALL GENETIC GAIN IF THAT VARIATE IS OMITTED
(2) THESE FIGURES ARE THE PERCENTAGES OF TOTAL GAIN ACCOUNTED FOR BY GAIN IN EACH TRAIT

INDEX 10 : INDIVIDUAL FEED EFF. OF BOARS AND PEN FEED EFF. OF SIBS DELETED FROM COMPLETE INDEX

	VARIATE		B-VALUE	VALUE OF VARIATE (1)
1	AV.D.GAIN	(B1)	0.4167	8.8268
2	B.FAT(PROBE)	(B1)	-0.5334	13.9848
3	AV.D.GAIN	(B2)	0.1008	0.4952
4	B.FAT(PROBE)	(B2)	-0.0875	0.3510
5	AV.B.FAT(CARC.)	(H+G)	-0.0272	0.0180
6	AV.DRESSING %	(H+G)	0.3222	3.3633
7	AV.% HAM+LOIN	(H+G)	0.3872	3.7122
8	AV. LOIN-EYE	(H+G)	0.2184	1.3172
9	AV.D.GAIN	(H+G)	0.2749	2.2120
10	AV. # WEANED		0.2027	2.3577

VARIANCE OF INDEX 0.8822
STD DEV OF INDEX 0.9393

VARIANCE OF AGG GENOT 4.9026
STD DEV OF AGG GENOT 2.2142

CORRELATION OF INDEX AND AGG GENOT 0.4242

REGRESSION OF EACH TRAIT ON INDEX, CORRELATION OF EACH TRAIT WITH INDEX, PERCENT OF ECONOMIC GAINS (2)

	TRAIT	REGRESSION	CORRELATION	PCT OF GAIN
1	AV.D.GAIN	0.1257	0.2156	9.0514
2	FEED EFF.	-0.2977	-0.4726	43.1611
3	B.FAT(CARCASS)	-0.3152	-0.4413	14.8774
4	DRESSING %	0.0150	0.0257	1.5102
5	% HAM + LOIN	0.2281	0.3194	18.5691
6	LOIN-EYE	0.2058	0.2607	8.1711
7	AV.#WEANED	0.0115	0.0341	4.6597

(1) VALUE OF EACH VARIATE IN THE INDEX IS PERCENT REDUCTION IN RATE OF OVERALL GENETIC GAIN IF THAT VARIATE IS OMITTED
(2) THESE FIGURES ARE THE PERCENTAGES OF TOTAL GAIN ACCOUNTED FOR BY GAIN IN EACH TRAIT

INDEX 11 : DAILY GAIN OF BOARS AND AV. DAILY GAIN OF SIBS DELETED FROM COMPLETE INDEX..

	VARIATE		B-VALUE	VALUE OF VARIATE (1)
1	FEED EFF.	(B1)	-0.7135	18.0971
2	B.FAT(PROBE)	(B1)	-0.2162	1.4690
3	FEED EFF.	(B2)	-0.1430	0.6638
4	B.FAT(PROBE)	(B2)	-0.0190	0.0113
5	AV.B.FAT(CARC.)	(H+G)	0.0117	0.0024
6	AV.DRESSING %	(H+G)	0.1675	0.6507
7	AV.% HAM+LOIN	(H+G)	0.2027	0.7224
8	AV. LOIN-EYE	(H+G)	0.2559	1.3384
9	AV.FEED EFF.	(H+G)	-0.1952	0.7124
10	AV. # WEANED		0.2027	1.7754

VARIANCE OF INDEX 1.1681
STD DEV OF INDEX 1.0808

VARIANCE OF AGG GENOT 4.9026
STD DEV OF AGG GENOT 2.2142

CORRELATION OF INDEX AND AGG GENOT 0.4881

REGRESSION OF EACH TRAIT ON INDEX, CORRELATION OF EACH TRAIT WITH INDEX, PERCENT OF ECONOMIC GAINS (2)

	TRAIT	REGRESSION	CORRELATION	PCT OF GAIN
1	AV.D.GAIN	0.1371	0.2705	9.8705
2	FEED EFF.	-0.3142	-0.5741	45.5637
3	B.FAT(CARCASS)	-0.2274	-0.3663	10.7318
4	DRESSING %	0.0616	0.1215	6.1937
5	% HAM + LOIN	0.2170	0.3496	17.6651
6	LOIN-EYE	0.1626	0.2370	6.4560
7	AV.#WEANED	0.0087	0.0297	3.5192

(1) VALUE OF EACH VARIATE IN THE INDEX IS PERCENT REDUCTION IN RATE OF OVERALL GENETIC GAIN IF THAT VARIATE IS OMITTED
(2) THESE FIGURES ARE THE PERCENTAGES OF TOTAL GAIN ACCOUNTED FOR BY GAIN IN EACH TRAIT

INDEX 12 : PROBE OF BOARS AND AV. CARCASS BACKFAT OF SIBS
DELETED FROM COMPLETE INDEX

	VARIATE		B-VALUE	VALUE OF VARIATE (1)
1	AV.D.GAIN	(B1)	-0.2351	1.3094
2	FEED EFF.	(B1)	-0.9323	22.5134
3	AV.D.GAIN	(B2)	-0.0415	0.0405
4	FEED EFF.	(B2)	-0.1769	0.7220
5	AV.DRESSING %	(H+G)	0.1492	0.5202
6	AV.% HAM+LOIN	(H+G)	0.2368	0.8279
7	AV. LOIN-EYE	(H+G)	0.2470	1.2831
8	AV.D.GAIN	(H+G)	0.1228	0.1592
9	AV.FEED EFF.	(H+G)	-0.1142	0.1242
10	AV. # WEANED		0.2027	1.7869

VARIANCE OF INDEX 1.1606
STD DEV OF INDEX 1.0773

VARIANCE OF AGG GENOT 4.9026
STD DEV OF AGG GENOT 2.2142

CORRELATION OF INDEX AND AGG GENOT 0.4866

REGRESSION OF EACH TRAIT ON INDEX, CORRELATION OF EACH TRAIT WITH INDEX, PERCENT OF ECONOMIC GAINS (2)

	TRAIT	REGRESSION	CORRELATION	PCT OF GAIN
1	AV.D.GAIN	0.1385	0.2724	9.9705
2	FEED EFF.	-0.3111	-0.5665	45.1078
3	B.FAT(CARCASS)	-0.1810	-0.2907	8.5439
4	DRESSING %	0.0853	0.1677	8.5769
5	% HAM + LOIN	0.2215	0.3557	18.0299
6	LOIN-EYE	0.1569	0.2279	6.2293
7	AV.#WEANED	0.0087	0.0298	3.5419

(1) VALUE OF EACH VARIATE IN THE INDEX IS PERCENT REDUCTION IN RATE OF OVERALL GENETIC GAIN IF THAT VARIATE IS OMITTED
(2) THESE FIGURES ARE THE PERCENTAGES OF TOTAL GAIN ACCOUNTED FOR BY GAIN IN EACH TRAIT

INDEX 13 : PROBE OF BOARS DELETED FROM COMPLETE INDEX

	VARIATE		B-VALUE	VALUE OF VARIATE (1)
1	AV.D.GAIN	(B1)	-0.2308	1.2539
2	FEED EFF.	(B1)	-0.9279	22.1214
3	AV.D.GAIN	(B2)	-0.0371	0.0323
4	FEED EFF.	(B2)	-0.1725	0.6826
5	AV.B.FAT(CARC.)	(H+G)	-0.0971	0.1636
6	AV.DRESSING %	(H+G)	0.1847	0.6744
7	AV.% HAM+LOIN	(H+G)	0.2311	0.7836
8	AV. LOIN-EYE	(H+G)	0.2282	1.0442
9	AV.D.GAIN	(H+G)	0.1711	0.2680
10	AV.FEED EFF.	(H+G)	-0.0535	0.0224
11	AV. # WEANED		0.2027	1.7810

VARIANCE OF INDEX 1.1644
STD DEV OF INDEX 1.0791

VARIANCE OF AGG GENOT 4.9026
STD DEV OF AGG GENOT 2.2142

CORRELATION OF INDEX AND AGG GENOT 0.4874

REGRESSION OF EACH TRAIT ON INDEX, CORRELATION OF EACH TRAIT WITH INDEX, PERCENT OF ECONOMIC GAINS (2)

	TRAIT	REGRESSION	CORRELATION	PCT OF GAIN
1	AV.D.GAIN	0.1368	0.2695	9.8478
2	FEED EFF.	-0.3110	-0.5672	45.0898
3	B.FAT(CARCASS)	-0.1905	-0.3064	8.9917
4	DRESSING %	0.0840	0.1655	8.4484
5	% HAM + LOIN	0.2202	0.3542	17.9243
6	LOIN-EYE	0.1554	0.2261	6.1677
7	AV.#WEANED	0.0087	0.0297	3.5303

(1) VALUE OF EACH VARIATE IN THE INDEX IS PERCENT REDUCTION IN RATE OF OVERALL GENETIC GAIN IF THAT VARIATE IS OMITTED
(2) THESE FIGURES ARE THE PERCENTAGES OF TOTAL GAIN ACCOUNTED FOR BY GAIN IN EACH TRAIT

INDEX 14 : AV. CARCASS BACKFAT OF SIBS DELETED FROM COMPLETE INDEX

	VARIATE		B-VALUE	VALUE OF VARIATE (1)
1	AV.D.GAIN	(B1)	-0.1378	0.3420
2	FEED EFF.	(B1)	-0.8139	11.1631
3	B.FAT(PROBE)	(B1)	-0.1698	0.7254
4	AV.D.GAIN	(B2)	-0.0219	0.0086
5	FEED EFF.	(B2)	-0.1560	0.3879
6	B.FAT(PROBE)	(B2)	-0.0206	0.0106
7	AV.DRESSING %	(H+G)	0.1824	0.7354
8	AV.% HAM+LOIN	(H+G)	0.2379	0.8217
9	AV. LOIN-EYE	(H+G)	0.2456	1.2475
10	AV.D.GAIN	(H+G)	0.1507	0.2328
11	AV.FEED EFF.	(H+G)	-0.0868	0.0697
12	AV. # WEANED		0.2027	1.7567

VARIANCE OF INDEX 1.1804
STD DEV OF INDEX 1.0865

VARIANCE OF AGG GENOT 4.9026
STD DEV OF AGG GENOT 2.2142

CORRELATION OF INDEX AND AGG GENOT 0.4907

REGRESSION OF EACH TRAIT ON INDEX, CORRELATION OF EACH TRAIT WITH INDEX, PERCENT OF ECONOMIC GAINS (2)

	TRAIT	REGRESSION	CORRELATION	PCT OF GAIN
1	AV.D.GAIN	0.1284	0.2548	9.2477
2	FEED EFF.	-0.3099	-0.5690	44.9294
3	B.FAT(CARCASS)	-0.2220	-0.3596	10.4791
4	DRESSING %	0.0699	0.1386	7.0291
5	% HAM + LOIN	0.2247	0.3639	18.2874
6	LOIN-EYE	0.1649	0.2415	6.5447
7	AV.#WEANED	0.0086	0.0295	3.4824

(1) VALUE OF EACH VARIATE IN THE INDEX IS PERCENT REDUCTION IN RATE OF OVERALL GENETIC GAIN IF THAT VARIATE IS OMITTED
(2) THESE FIGURES ARE THE PERCENTAGES OF TOTAL GAIN ACCOUNTED FOR BY GAIN IN EACH TRAIT

INDEX 15 : AV. PERCENT HAM AND LOIN OF SIBS DELETED FROM COMPLETE INDEX

	VARIATE		B-VALUE	VALUE OF VARIATE (1)
1	AV.D.GAIN	(B1)	-0.1491	0.4062
2	FEED EFF.	(B1)	-0.8254	11.6295
3	B.FAT(PROBE)	(B1)	-0.1607	0.6286
4	AV.D.GAIN	(B2)	-0.0332	0.0201
5	FEED EFF.	(B2)	-0.1675	0.4522
6	B.FAT(PROBE)	(B2)	-0.0114	0.0032
7	AV.B.FAT(CARC.)	(H+G)	-0.0495	0.0377
8	AV.DRESSING %	(H+G)	0.1668	0.5589
9	AV. LOIN-EYE	(H+G)	0.3318	2.8190
10	AV.D.GAIN	(H+G)	0.0532	0.0303
11	AV.FEED EFF.	(H+G)	-0.2034	0.3952
12	AV. # WEANED		0.2027	1.7848

VARIANCE OF INDEX 1.1620
STD DEV OF INDEX 1.0780

VARIANCE OF AGG GENOT 4.9026
STD DEV OF AGG GENOT 2.2142

CORRELATION OF INDEX AND AGG GENOT 0.4868

REGRESSION OF EACH TRAIT ON INDEX, CORRELATION OF EACH TRAIT WITH INDEX, PERCENT OF ECONOMIC GAINS (2)

	TRAIT	REGRESSION	CORRELATION	PCT OF GAIN
1	AV.D.GAIN	0.1331	0.2620	9.5861
2	FEED EFF.	-0.3141	-0.5724	45.5502
3	B.FAT(CARCASS)	-0.2282	-0.3668	10.7731
4	DRESSING %	0.0704	0.1385	7.0791
5	% HAM + LOIN	0.2076	0.3337	16.9015
6	LOIN-EYE	0.1655	0.2406	6.5722
7	AV.#WEANED	0.0087	0.0297	3.5377

(1) VALUE OF EACH VARIATE IN THE INDEX IS PERCENT REDUCTION IN RATE OF OVERALL GENETIC GAIN IF THAT VARIATE IS OMITTED
(2) THESE FIGURES ARE THE PERCENTAGES OF TOTAL GAIN ACCOUNTED FOR BY GAIN IN EACH TRAIT

INDEX 16 : AV. LOIN-EYE OF SIBS DELETED FROM COMPLETE INDEX

	VARIATE		B-VALUE	VALUE OF VARIATE (1)
1	AV.D.GAIN	(B1)	-0.1442	0.3817
2	FEED EFF.	(B1)	-0.8223	11.6025
3	B.FAT(PROBE)	(B1)	-0.1545	0.5851
4	AV.D.GAIN	(B2)	-0.0283	0.0147
5	FEED EFF.	(B2)	-0.1644	0.4378
6	B.FAT(PROBE)	(B2)	-0.0052	0.0007
7	AV.B.FAT(CARC.)	(H+G)	-0.0949	0.1460
8	AV.DRESSING %	(H+G)	0.2543	1.3795
9	AV.% HAM+LOIN	(H+G)	0.3638	2.5058
10	AV.D.GAIN	(H+G)	0.2227	0.4698
11	AV.FEED EFF.	(H+G)	0.0143	0.0017
12	AV. # WEANED		0.2027	1.7964

VARIANCE OF INDEX 1.1545
STD DEV OF INDEX 1.0745

VARIANCE OF AGG GENOT 4.9026
STD DEV OF AGG GENOT 2.2142

CORRELATION OF INDEX AND AGG GENOT 0.4853

REGRESSION OF EACH TRAIT ON INDEX, CORRELATION OF EACH TRAIT WITH INDEX, PERCENT OF ECONOMIC GAINS (2)

	TRAIT	REGRESSION	CORRELATION	PCT OF GAIN
1	AV.D.GAIN	0.1314	0.2577	9.4582
2	FEED EFF.	-0.3166	-0.5749	45.9009
3	B.FAT(CARCASS)	-0.2237	-0.3584	10.5604
4	DRESSING %	0.0721	0.1414	7.2524
5	% HAM + LOIN	0.2231	0.3573	18.1587
6	LOIN-EYE	0.1287	0.1864	5.1089
7	AV.#WEANED	0.0088	0.0298	3.5605

(1) VALUE OF EACH VARIATE IN THE INDEX IS PERCENT REDUCTION IN RATE OF OVERALL GENETIC GAIN IF THAT VARIATE IS OMITTED
(2) THESE FIGURES ARE THE PERCENTAGES OF TOTAL GAIN ACCOUNTED FOR BY GAIN IN EACH TRAIT

INDEX 17 : AV. PERCENT HAM AND LOIN AND AV. LOIN-EYE OF SIBS DELETED FROM COMPLETE INDEX

	VARIATE		B-VALUE	VALUE OF VARIATE (1)
1	AV.D.GAIN	(B1)	-0.1654	0.5302
2	FEED EFF.	(B1)	-0.8434	12.9729
3	B.FAT(PROBE)	(B1)	-0.1417	0.5185
4	AV.D.GAIN	(B2)	-0.0495	0.0474
5	FEED EFF.	(B2)	-0.1855	0.5886
6	B.FAT(PROBE)	(B2)	0.0076	0.0015
7	AV.B.FAT(CARC.)	(H+G)	-0.1667	0.4912
8	AV.DRESSING %	(H+G)	0.2488	1.3899
9	AV.D.GAIN	(H+G)	0.0429	0.0210
10	AV.FEED EFF.	(H+G)	-0.1932	0.3776
11	AV. # WEANED		0.2027	1.8909

VARIANCE OF INDEX 1.0974
STD DEV OF INDEX 1.0476

VARIANCE OF AGG GENOT 4.9026
STD DEV OF AGG GENOT 2.2142

CORRELATION OF INDEX AND AGG GENOT 0.4731

REGRESSION OF EACH TRAIT ON INDEX, CORRELATION OF EACH TRAIT WITH INDEX, PERCENT OF ECONOMIC GAINS (2)

	TRAIT	REGRESSION	CORRELATION	PCT OF GAIN
1	AV.D.GAIN	0.1440	0.2754	10.3681
2	FEED EFF.	-0.3311	-0.5863	48.0093
3	B.FAT(CARCASS)	-0.2341	-0.3655	11.0479
4	DRESSING %	0.0742	0.1418	7.4606
5	% HAM + LOIN	0.1882	0.2939	15.3179
6	LOIN-EYE	0.1020	0.1441	4.0503
7	AV.#WEANED	0.0092	0.0306	3.7459

(1) VALUE OF EACH VARIATE IN THE INDEX IS PERCENT REDUCTION IN RATE OF OVERALL GENETIC GAIN IF THAT VARIATE IS OMITTED
(2) THESE FIGURES ARE THE PERCENTAGES OF TOTAL GAIN ACCOUNTED FOR BY GAIN IN EACH TRAIT

INDEX 18 : AV. DAILY GAIN, AV. FEED EFF., PROBE AND US LOIN-EYE ON THE TWO BOARS

	VARIATE		B-VALUE	VALUE OF VARIATE (1)
1	AV.D.GAIN	(B1)	-0.0897	0.1425
2	FEED EFF.	(B1)	-0.8303	11.5314
3	B.FAT(PROBE)	(B1)	-0.1001	0.2411
4	AV.D.GAIN	(B2)	-0.0276	0.0136
5	FEED EFF.	(B2)	-0.2195	0.7623
6	B.FAT(PROBE)	(B2)	-0.0224	0.0121
7	US. LOIN EYE	(B1)	0.5036	8.6591
8	US. LOIN EYE	(B2)	0.0652	0.1389

VARIANCE OF INDEX 1.2343
STD DEV OF INDEX 1.1110

VARIANCE OF AGG GENOT 4.9026
STD DEV OF AGG GENOT 2.2142

CORRELATION OF INDEX AND AGG GENOT 0.5018

REGRESSION OF EACH TRAIT ON INDEX, CORRELATION OF EACH TRAIT WITH INDEX, PERCENT OF ECONOMIC GAINS (2)

	TRAIT	REGRESSION	CORRELATION	PCT OF GAIN
1	AV.D.GAIN	0.1099	0.2229	7.9108
2	FEED EFF.	-0.2863	-0.5377	41.5139
3	B.FAT(CARCASS)	-0.2241	-0.3711	10.5770
4	DRESSING %	0.0700	0.1420	7.0447
5	% HAM + LOIN	0.2581	0.4275	21.0133
6	LOIN-EYE	0.3008	0.4506	11.9403
7	AV.#WEANED	0.0	0.0	0.0

(1) VALUE OF EACH VARIATE IN THE INDEX IS PERCENT REDUCTION IN RATE OF OVERALL GENETIC GAIN IF THAT VARIATE IS OMITTED
(2) THESE FIGURES ARE THE PERCENTAGES OF TOTAL GAIN ACCOUNTED FOR BY GAIN IN EACH TRAIT

INDEX 19 : AV. DAILY GAIN AND PROBE ON BOAR 1 WITH PEN FEED EFF.

	VARIATE		B-VALUE	VALUE OF VARIATE (1)
1	AV.D.GAIN	(B1)	0.0789	0.2446
2	B.FAT(PROBE)	(B1)	-0.3442	5.8190
3	AV.FEED EFF.	(B1+B2)	-0.9078	21.6497

VARIANCE OF INDEX 0.8420
STD DEV OF INDEX 0.9176

VARIANCE OF AGG GENOT 4.9026
STD DEV OF AGG GENOT 2.2142

CORRELATION OF INDEX AND AGG GENOT 0.4144

REGRESSION OF EACH TRAIT ON INDEX, CORRELATION OF EACH TRAIT WITH INDEX, PERCENT OF ECONOMIC GAINS (2)

	TRAIT	REGRESSION	CORRELATION	PCT OF GAIN
1	AV.D.GAIN	0.1758	0.2945	12.6558
2	FEED EFF.	-0.3645	-0.5654	52.8549
3	B.FAT(CARCASS)	-0.2991	-0.4092	14.1195
4	DRESSING %	0.0127	0.0212	1.2750
5	% HAM + LOIN	0.1851	0.2531	15.0632
6	LOIN-EYE	0.1016	0.1256	4.0316
7	AV.#WEANED	0.0	0.0	0.0

(1) VALUE OF EACH VARIATE IN THE INDEX IS PERCENT REDUCTION IN RATE OF OVERALL GENETIC GAIN IF THAT VARIATE IS OMITTED
(2) THESE FIGURES ARE THE PERCENTAGES OF TOTAL GAIN ACCOUNTED FOR BY GAIN IN EACH TRAIT

INDEX 20 : AV. DAILY GAIN, PROBE AND FEED EFF. ON BOAR 1

	VARIATE		B-VALUE	VALUE OF VARIATE (1)
1	AV.D.GAIN	(B1)	-0.2001	1.0096
2	FEED EFF.	(B1)	-0.9867	25.0753
3	B.FAT(PROBE)	(B1)	-0.1658	0.9881

VARIANCE OF INDEX 0.9207
STD DEV OF INDEX 0.9596

VARIANCE OF AGG GENOT 4.9026
STD DEV OF AGG GENOT 2.2142

CORRELATION OF INDEX AND AGG GENOT 0.4334

REGRESSION OF EACH TRAIT ON INDEX, CORRELATION OF EACH TRAIT WITH INDEX, PERCENT OF ECONOMIC GAINS (2)

	TRAIT	REGRESSION	CORRELATION	PCT OF GAIN
1	AV.D.GAIN	0.1583	0.2774	11.3987
2	FEED EFF.	-0.3541	-0.5743	51.3380
3	B.FAT(CARCASS)	-0.2535	-0.3627	11.9672
4	DRESSING %	0.0500	0.0876	5.0309
5	% HAM + LOIN	0.1996	0.2855	16.2488
6	LOIN-EYE	0.1012	0.1309	4.0163
7	AV.#WEANED	0.0	0.0	0.0

(1) VALUE OF EACH VARIATE IN THE INDEX IS PERCENT REDUCTION IN RATE OF OVERALL GENETIC GAIN IF THAT VARIATE IS OMITTED
(2) THESE FIGURES ARE THE PERCENTAGES OF TOTAL GAIN ACCOUNTED FOR BY GAIN IN EACH TRAIT

INDEX 21 : AV. DAILY GAIN, PROBE, FEED EFF. AND US LOIN-EYE ON BOAR 1

	VARIATE		B-VALUE	VALUE OF VARIATE (1)
1	AV.D.GAIN	(B1)	-0.0933	0.1666
2	FEED EFF.	(B1)	-0.8867	14.6145
3	B.FAT(PROBE)	(B1)	-0.1107	0.3385
4	US. LOIN EYE	(B1)	0.5305	11.8663

VARIANCE OF INDEX 1.1854
STD DEV OF INDEX 1.0887

VARIANCE OF AGG GENOT 4.9026
STD DEV OF AGG GENOT 2.2142

CORRELATION OF INDEX AND AGG GENOT 0.4917

REGRESSION OF EACH TRAIT ON INDEX, CORRELATION OF EACH TRAIT WITH INDEX, PERCENT OF ECONOMIC GAINS (2)

	TRAIT	REGRESSION	CORRELATION	PCT OF GAIN
1	AV.D.GAIN	0.1075	0.2137	7.7396
2	FEED EFF.	-0.2839	-0.5225	41.1716
3	B.FAT(CARCASS)	-0.2252	-0.3654	10.6271
4	DRESSING %	0.0701	0.1393	7.0514
5	% HAM + LOIN	0.2605	0.4227	21.2022
6	LOIN-EYE	0.3075	0.4514	12.2080
7	AV.#WEANED	0.0	0.0	0.0

(1) VALUE OF EACH VARIATE IN THE INDEX IS PERCENT REDUCTION IN RATE OF OVERALL GENETIC GAIN IF THAT VARIATE IS OMITTED
(2) THESE FIGURES ARE THE PERCENTAGES OF TOTAL GAIN ACCOUNTED FOR BY GAIN IN EACH TRAIT

INDEX 22 : AV. DAILY GAIN, PROBE AND US LOIN-EYE ON BOAR 1
WITH PEN FEED EFF.

	VARIATE		B-VALUE	VALUE OF VARIATE (1)
1	AV.D.GAIN	(B1)	0.1522	0.6678
2	B.FAT(PROBE)	(B1)	-0.2614	2.4013
3	AV.FEED EFF.	(B1+B2)	-0.8319	12.7459
4	US. LOIN EYE	(B1)	0.5562	13.8752

VARIANCE OF INDEX 1.1351
STD DEV OF INDEX 1.0654

VARIANCE OF AGG GENOT 4.9026
STD DEV OF AGG GENOT 2.2142

CORRELATION OF INDEX AND AGG GENOT 0.4812

REGRESSION OF EACH TRAIT ON INDEX, CORRELATION OF EACH TRAIT WITH INDEX, PERCENT OF ECONOMIC GAINS (2)

	TRAIT	REGRESSION	CORRELATION	PCT OF GAIN
1	AV.D.GAIN	0.1142	0.2222	8.2237
2	FEED EFF.	-0.2841	-0.5117	41.1964
3	B.FAT(CARCASS)	-0.2511	-0.3988	11.8523
4	DRESSING %	0.0482	0.0937	4.8466
5	% HAM + LOIN	0.2567	0.4077	20.8939
6	LOIN-EYE	0.3271	0.4700	12.9872
7	AV.#WEANED	0.0	0.0	0.0

(1) VALUE OF EACH VARIATE IN THE INDEX IS PERCENT REDUCTION IN RATE OF OVERALL GENETIC GAIN IF THAT VARIATE IS OMITTED
(2) THESE FIGURES ARE THE PERCENTAGES OF TOTAL GAIN ACCOUNTED FOR BY GAIN IN EACH TRAIT

INDEX 23 : AV. DAILY GAIN AND PROBE ON BOARS 1 AND 2 WITH PEN FEED EFF.

	VARIATE		B-VALUE	VALUE OF VARIATE (1)
1	AV.D.GAIN	(B1)	0.0282	0.0280
2	B.FAT(PROBE)	(B1)	-0.3042	3.9072
3	AV.D.GAIN	(B2)	-0.2876	2.9543
4	B.FAT(PROBE)	(B2)	0.1417	0.8346
5	AV.FEED EFF.	(B1+B2)	-1.1838	22.1758

VARIANCE OF INDEX 0.8967
STD DEV OF INDEX 0.9469

VARIANCE OF AGG GENOT 4.9026
STD DEV OF AGG GENOT 2.2142

CORRELATION OF INDEX AND AGG GENOT 0.4277

REGRESSION OF EACH TRAIT ON INDEX, CORRELATION OF EACH TRAIT WITH INDEX, PERCENT OF ECONOMIC GAINS (2)

	TRAIT	REGRESSION	CORRELATION	PCT OF GAIN
1	AV.D.GAIN	0.1599	0.2764	11.5121
2	FEED EFF.	-0.3566	-0.5708	51.7053
3	B.FAT(CARCASS)	-0.2716	-0.3833	12.8178
4	DRESSING %	0.0380	0.0657	3.8230
5	% HAM + LOIN	0.1970	0.2782	16.0397
6	LOIN-EYE	0.1033	0.1319	4.1021
7	AV.#WEANED	0.0	0.0	0.0

(1) VALUE OF EACH VARIATE IN THE INDEX IS PERCENT REDUCTION IN RATE OF OVERALL GENETIC GAIN IF THAT VARIATE IS OMITTED
(2) THESE FIGURES ARE THE PERCENTAGES OF TOTAL GAIN ACCOUNTED FOR BY GAIN IN EACH TRAIT

INDEX 24 : AV. DAILY GAIN, PROBE AND US LOIN-EYE ON BOARS 1 AND 2 WITH PEN FEED EFF.

	VARIATE		B-VALUE	VALUE OF VARIATE (1)
1	AV.D.GAIN	(B1)	0.1131	0.3391
2	B.FAT(PROBE)	(B1)	-0.2349	1.7125
3	AV.D.GAIN	(B2)	-0.2276	1.3797
4	B.FAT(PROBE)	(B2)	0.1106	0.3773
5	AV.FEED EFF.	(B1+B2)	-1.0458	12.2622
6	US. LOIN EYE	(B1)	0.5217	9.8952
7	US. LOIN EYE	(B2)	0.0475	0.0779

VARIANCE OF INDEX 1.1718
STD DEV OF INDEX 1.0825

VARIANCE OF AGG GENOT 4.9026
STD DEV OF AGG GENOT 2.2142

CORRELATION OF INDEX AND AGG GENOT 0.4889

REGRESSION OF EACH TRAIT ON INDEX, CORRELATION OF EACH TRAIT WITH INDEX, PERCENT OF ECONOMIC GAINS (2)

	TRAIT	REGRESSION	CORRELATION	PCT OF GAIN
1	AV.D.GAIN	0.1073	0.2121	7.7277
2	FEED EFF.	-0.2833	-0.5184	41.0767
3	B.FAT(CARCASS)	-0.2380	-0.3841	11.2345
4	DRESSING %	0.0613	0.1211	6.1625
5	% HAM + LOIN	0.2605	0.4204	21.2064
6	LOIN-EYE	0.3172	0.4630	12.5922
7	AV.#WEANED	0.0	0.0	0.0

(1) VALUE OF EACH VARIATE IN THE INDEX IS PERCENT REDUCTION IN RATE OF OVERALL GENETIC GAIN IF THAT VARIATE IS OMITTED
(2) THESE FIGURES ARE THE PERCENTAGES OF TOTAL GAIN ACCOUNTED FOR BY GAIN IN EACH TRAIT

INDEX 25 : AV. DAILY GAIN AND PROBE ON BOAR 1 WITH PEN FEED EFF. AND COMPLETE INFORMATION ON SIBS

	VARIATE		B-VALUE	VALUE OF VARIATE (1)
1	AV.D.GAIN	(B1)	0.1351	0.5558
2	B.FAT(PROBE)	(B1)	-0.3501	4.3849
3	AV.FEED EFF.	(B1+B2)	-0.7289	9.2776
4	AV.B.FAT(CARC.)	(H+G)	0.0091	0.0015
5	AV.DRESSING %	(H+G)	0.2104	0.9902
6	AV.% HAM+LOIN	(H+G)	0.2521	1.0568
7	AV. LOIN-EYE	(H+G)	0.2477	1.3876
8	AV.D.GAIN	(H+G)	0.1047	0.1167
9	AV.FEED EFF.	(H+G)	-0.1056	0.0990

VARIANCE OF INDEX 1.0311
STD DEV OF INDEX 1.0154

VARIANCE OF AGG GENOT 4.9026
STD DEV OF AGG GENOT 2.2142

CORRELATION OF INDEX AND AGG GENOT 0.4586

REGRESSION OF EACH TRAIT ON INDEX, CORRELATION OF EACH TRAIT WITH INDEX, PERCENT OF ECONOMIC GAINS (2)

	TRAIT	REGRESSION	CORRELATION	PCT OF GAIN
1	AV.D.GAIN	0.1374	0.2548	9.8952
2	FEED EFF.	-0.3220	-0.5527	46.6948
3	B.FAT(CARCASS)	-0.2639	-0.3994	12.4541
4	DRESSING %	0.0502	0.0931	5.0522
5	% HAM + LOIN	0.2292	0.3469	18.6562
6	LOIN-EYE	0.1826	0.2500	7.2475
7	AV.#WEANED	0.0	0.0	0.0

(1) VALUE OF EACH VARIATE IN THE INDEX IS PERCENT REDUCTION IN RATE OF OVERALL GENETIC GAIN IF THAT VARIATE IS OMITTED
(2) THESE FIGURES ARE THE PERCENTAGES OF TOTAL GAIN ACCOUNTED FOR BY GAIN IN EACH TRAIT

INDEX 26 : AV. DAILY GAIN AND PROBE ON BOAR 1 WITH PEN FEED EFF. AND CARCASS INFORMATION ON SIBS

	VARIATE		B-VALUE	VALUE OF VARIATE (1)
1	AV.D.GAIN	(B1)	0.1545	0.7604
2	B.FAT(PROBE)	(B1)	-0.3396	4.2146
3	AV.FEED EFF.	(B1+B2)	-0.7902	12.4015
4	AV.B.FAT(CARC.)	(H+G)	-0.0083	0.0016
5	AV.DRESSING %	(H+G)	0.2189	1.3278
6	AV.% HAM+LOIN	(H+G)	0.2627	1.4587
7	AV. LOIN-EYE	(H+G)	0.2337	1.3163

VARIANCE OF INDEX 1.0125
STD DEV OF INDEX 1.0062

VARIANCE OF AGG GENOT 4.9026
STD DEV OF AGG GENOT 2.2142

CORRELATION OF INDEX AND AGG GENOT 0.4544

REGRESSION OF EACH TRAIT ON INDEX, CORRELATION OF EACH TRAIT WITH INDEX, PERCENT OF ECONOMIC GAINS (2)

	TRAIT	REGRESSION	CORRELATION	PCT OF GAIN
1	AV.D.GAIN	0.1289	0.2368	9.2791
2	FEED EFF.	-0.3187	-0.5420	46.2075
3	B.FAT(CARCASS)	-0.2684	-0.4026	12.6671
4	DRESSING %	0.0532	0.0977	5.3506
5	% HAM + LOIN	0.2351	0.3526	19.1366
6	LOIN-EYE	0.1854	0.2515	7.3591
7	AV.#WEANED	0.0	0.0	0.0

(1) VALUE OF EACH VARIATE IN THE INDEX IS PERCENT REDUCTION IN RATE OF OVERALL GENETIC GAIN IF THAT VARIATE IS OMITTED
(2) THESE FIGURES ARE THE PERCENTAGES OF TOTAL GAIN ACCOUNTED FOR BY GAIN IN EACH TRAIT

INDEX 27 : AV. DAILY GAIN, FEED EFF. AND PROBE ON BOAR 1
WITH COMPLETE INFORMATION ON SIBS

	VARIATE		B-VALUE	VALUE OF VARIATE (1)
1	AV.D.GAIN	(B1)	-0.1419	0.3884
2	FEED EFF.	(B1)	-0.8426	12.9617
3	B.FAT(PROBE)	(B1)	-0.1685	0.7495
4	AV.B.FAT(CARC.)	(H+G)	-0.0465	0.0362
5	AV.DRESSING %	(H+G)	0.1953	0.7842
6	AV.% HAM+LOIN	(H+G)	0.2402	0.8815
7	AV. LOIN-EYE	(H+G)	0.2377	1.1754
8	AV.D.GAIN	(H+G)	0.1642	0.2627
9	AV.FEED EFF.	(H+G)	-0.1159	0.1119

VARIANCE OF INDEX 1.1202
STD DEV OF INDEX 1.0584

VARIANCE OF AGG GENOT 4.9026
STD DEV OF AGG GENOT 2.2142

CORRELATION OF INDEX AND AGG GENOT 0.4780

REGRESSION OF EACH TRAIT ON INDEX, CORRELATION OF EACH TRAIT WITH INDEX, PERCENT OF ECONOMIC GAINS (2)

	TRAIT	REGRESSION	CORRELATION	PCT OF GAIN
1	AV.D.GAIN	0.1317	0.2545	9.4837
2	FEED EFF.	-0.3201	-0.5726	46.4107
3	B.FAT(CARCASS)	-0.2327	-0.3671	10.9830
4	DRESSING %	0.0726	0.1404	7.3072
5	% HAM + LOIN	0.2334	0.3683	18.9992
6	LOIN-EYE	0.1717	0.2450	6.8162
7	AV.#WEANED	0.0	0.0	0.0

(1) VALUE OF EACH VARIATE IN THE INDEX IS PERCENT REDUCTION IN RATE OF OVERALL GENETIC GAIN IF THAT VARIATE IS OMITTED
(2) THESE FIGURES ARE THE PERCENTAGES OF TOTAL GAIN ACCOUNTED FOR BY GAIN IN EACH TRAIT

INDEX 28 : AV. DAILY GAIN, PROBE AND FEED EFF. ON BOAR 1
WITH CARCASS INFORMATION ON SIBS

	VARIATE		B-VALUE	VALUE OF VARIATE (1)
1	AV.D.GAIN	(B1)	-0.1048	0.2257
2	FEED EFF.	(B1)	-0.8801	15.3656
3	B.FAT(PROBE)	(B1)	-0.1591	0.6918
4	AV.B.FAT(CARC.)	(H+G)	-0.0661	0.0925
5	AV.DRESSING %	(H+G)	0.2035	1.0681
6	AV.% HAM+LOIN	(H+G)	0.2507	1.2393
7	AV. LOIN-EYE	(H+G)	0.2205	1.0935

VARIANCE OF INDEX 1.0846
STD DEV OF INDEX 1.0415

VARIANCE OF AGG GENOT 4.9026
STD DEV OF AGG GENOT 2.2142

CORRELATION OF INDEX AND AGG GENOT 0.4704

REGRESSION OF EACH TRAIT ON INDEX, CORRELATION OF EACH TRAIT WITH INDEX, PERCENT OF ECONOMIC GAINS (2)

	TRAIT	REGRESSION	CORRELATION	PCT OF GAIN
1	AV.D.GAIN	0.1196	0.2275	8.6129
2	FEED EFF.	-0.3154	-0.5551	45.7266
3	B.FAT(CARCASS)	-0.2395	-0.3718	11.3025
4	DRESSING %	0.0764	0.1453	7.6893
5	% HAM + LOIN	0.2417	0.3752	19.6742
6	LOIN-EYE	0.1762	0.2474	6.9946
7	AV.#WEANED	0.0	0.0	0.0

(1) VALUE OF EACH VARIATE IN THE INDEX IS PERCENT REDUCTION IN RATE OF OVERALL GENETIC GAIN IF THAT VARIATE IS OMITTED
(2) THESE FIGURES ARE THE PERCENTAGES OF TOTAL GAIN ACCOUNTED FOR BY GAIN IN EACH TRAIT

IX. APPENDIX B: CONSTITUENT INDEXES OF MAIN INDEX

SUBINDEXES OF COMPLETE INDEX

SUBINDEX FOR TRAIT : AV.D.GAIN

VARIANCE OF SUBINDEX 0.1096
CORRELATION OF SUBINDEX AND TRAIT 0.6045

	VARIATE		B-VALUE	VALUE OF VARIATE
1	AV.D.GAIN	(B1)	0.1804	6.4850
2	FEED EFF.	(B1)	-0.1052	1.9025
3	B.FAT(PROBE)	(B1)	0.0763	1.5095
4	AV.D.GAIN	(B2)	0.0433	0.3617
5	FEED EFF.	(B2)	-0.0146	0.0365
6	B.FAT(PROBE)	(B2)	0.0092	0.0219
7	AV.B.FAT(CARC.)	(H+G)	0.0077	0.0097
8	AV.DRESSING %	(H+G)	-0.0328	0.2246
9	AV.% HAM+LOIN	(H+G)	-0.0398	0.2461
10	AV. LOIN-EYE	(H+G)	-0.0013	0.0004
11	AV.D.GAIN	(H+G)	0.0642	0.4003
12	AV.FEED EFF.	(H+G)	-0.0564	0.2637
13	AV. # WEANED		0.0	0.0

SUBINDEX FOR TRAIT : FEED EFF.

VARIANCE OF SUBINDEX 0.1379
CORRELATION OF SUBINDEX AND TRAIT 0.6278

	VARIATE		B-VALUE	VALUE OF VARIATE
1	AV.D.GAIN	(B1)	-0.0296	0.1348
2	FEED EFF.	(B1)	0.2687	10.2900
3	B.FAT(PROBE)	(B1)	0.0393	0.3156
4	AV.D.GAIN	(B2)	-0.0029	0.0013
5	FEED EFF.	(B2)	0.0569	0.4393
6	B.FAT(PROBE)	(B2)	-0.0004	0.0001
7	AV.B.FAT(CARC.)	(H+G)	0.0132	0.0224
8	AV.DRESSING %	(H+G)	-0.0062	0.0063
9	AV.% HAM+LOIN	(H+G)	-0.0113	0.0159
10	AV. LOIN-EYE	(H+G)	-0.0042	0.0029
11	AV.D.GAIN	(H+G)	-0.0191	0.0281
12	AV.FEED EFF.	(H+G)	0.0976	0.6284
13	AV. # WEANED		0.0	0.0

SUBINDEX FOR TRAIT : B.FAT(CARCASS)

VARIANCE OF SUBINDEX 0.2213
CORRELATION OF SUBINDEX AND TRAIT 0.7013

	VARIATE		B-VALUE	VALUE OF VARIATE
1	AV.D.GAIN	(B1)	-0.0355	0.1203
2	FEED EFF.	(B1)	-0.0365	0.1125
3	B.FAT(PROBE)	(B1)	0.4091	24.2493
4	AV.D.GAIN	(B2)	-0.0139	0.0183
5	FEED EFF.	(B2)	-0.0129	0.0141
6	B.FAT(PROBE)	(B2)	0.0657	0.5513
7	AV.B.FAT(CARC.)	(H+G)	0.1360	1.5002
8	AV.DRESSING %	(H+G)	-0.0055	0.0032
9	AV.% HAM+LOIN	(H+G)	0.0175	0.0236
10	AV. LOIN-EYE	(H+G)	-0.0498	0.2597
11	AV.D.GAIN	(H+G)	-0.0120	0.0070
12	AV.FEED EFF.	(H+G)	-0.0059	0.0015
13	AV. # WEANED		0.0	0.0

SUBINDEX FOR TRAIT : DRESSING %

VARIANCE OF SUBINDEX 0.0574
CORRELATION OF SUBINDEX AND TRAIT 0.4374

	VARIATE		B-VALUE	VALUE OF VARIATE
1	AV.D.GAIN	(B1)	-0.1742	11.8766
2	FEED EFF.	(B1)	-0.1987	13.7792
3	B.FAT(PROBE)	(B1)	0.1440	10.7661
4	AV.D.GAIN	(B2)	-0.0403	0.6004
5	FEED EFF.	(B2)	-0.0446	0.6483
6	B.FAT(PROBE)	(B2)	0.0283	0.3950
7	AV.B.FAT(CARC.)	(H+G)	-0.0296	0.2725
8	AV.DRESSING %	(H+G)	0.2185	21.2932
9	AV.% HAM+LOIN	(H+G)	0.0136	0.0547
10	AV. LOIN-EYE	(H+G)	-0.0034	0.0046
11	AV.D.GAIN	(H+G)	0.0299	0.1656
12	AV.FEED EFF.	(H+G)	0.0476	0.3581
13	AV. # WEANED		0.0	0.0

SUBINDEX FOR TRAIT : % HAM + LOIN

VARIANCE OF SUBINDEX 0.1210
CORRELATION OF SUBINDEX AND TRAIT 0.5185

	VARIATE		B-VALUE	VALUE OF VARIATE
1	AV.D.GAIN	(B1)	-0.1625	4.7243
2	FEED EFF.	(B1)	-0.1878	5.5950
3	B.FAT(PROBE)	(B1)	-0.0814	1.5546
4	AV.C.GAIN	(B2)	-0.0328	0.1883
5	FEED EFF.	(B2)	-0.0371	0.2125
6	B.FAT(PROBE)	(B2)	-0.0071	0.0118
7	AV.B.FAT(CARC.)	(H+G)	0.0474	0.3312
8	AV.DRESSING %	(H+G)	-0.0043	0.0034
9	AV.% HAM+LOIN	(H+G)	0.2908	12.6988
10	AV. LOIN-EYE	(H+G)	0.0638	0.7798
11	AV.C.GAIN	(H+G)	0.0609	0.3265
12	AV.FEED EFF.	(H+G)	0.0757	0.4303
13	AV. # WEANED		0.0	0.0

SUBINDEX FOR TRAIT : LOIN-EYE

VARIANCE OF SUBINDEX 0.1316
CORRELATION OF SUBINDEX AND TRAIT 0.4891

	VARIATE		B-VALUE	VALUE OF VARIATE
1	AV.D.GAIN	(B1)	-0.0557	0.4998
2	FEED EFF.	(B1)	-0.0401	0.2287
3	B.FAT(PROBE)	(B1)	-0.1191	3.0850
4	AV.C.GAIN	(B2)	0.0032	0.0017
5	FEED EFF.	(B2)	0.0080	0.0090
6	B.FAT(PROBE)	(B2)	-0.0336	0.2426
7	AV.B.FAT(CARC.)	(H+G)	0.0833	0.9434
8	AV.DRESSING %	(H+G)	-0.0276	0.1321
9	AV.% HAM+LOIN	(H+G)	0.0146	0.0277
10	AV. LOIN-EYE	(H+G)	0.4073	35.4148
11	AV.D.GAIN	(H+G)	0.0192	0.0297
12	AV.FEED EFF.	(H+G)	0.0095	0.0062
13	AV. # WEANED		0.0	0.0

SUBINDEX FOR TRAIT : AV.#WEANED

VARIANCE OF SUBINDEX 0.0025
CORRELATION OF SUBINDEX AND TRAIT 0.1581

	VARIATE		B-VALUE	VALUE OF VARIATE
1	AV.D.GAIN	(B1)	0.0	0.0
2	FEED EFF.	(B1)	0.0	0.0
3	B.FAT(PROBE)	(B1)	0.0	0.0
4	AV.D.GAIN	(B2)	0.0	0.0
5	FEED EFF.	(B2)	0.0	0.0
6	B.FAT(PROBE)	(B2)	0.0	0.0
7	AV.B.FAT(CARC.)	(H+G)	0.0	0.0
8	AV.DRESSING %	(H+G)	0.0	0.0
9	AV.% HAM+LOIN	(H+G)	0.0	0.0
10	AV. LOIN-EYE	(H+G)	0.0	0.0
11	AV.D.GAIN	(H+G)	0.0	0.0
12	AV.FEED EFF.	(H+G)	0.0	0.0
13	AV. # WEANED		0.0500	100.0000